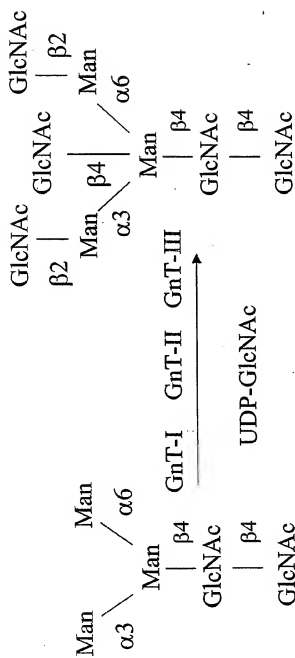


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Trimannosyl core with
Bisecting GlcNAc

FIG. 1

Trimannosyl core

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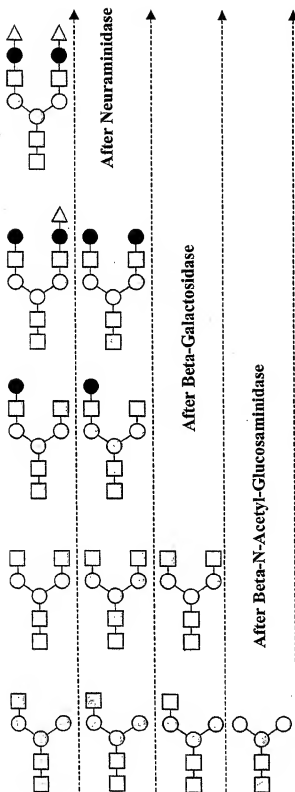
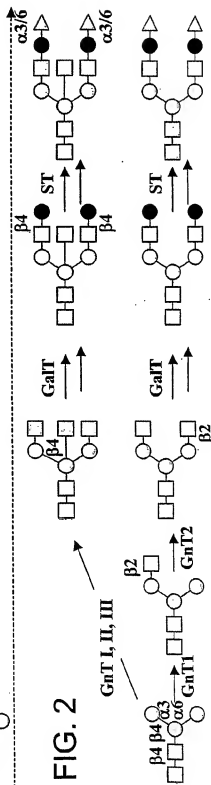


FIG. 2



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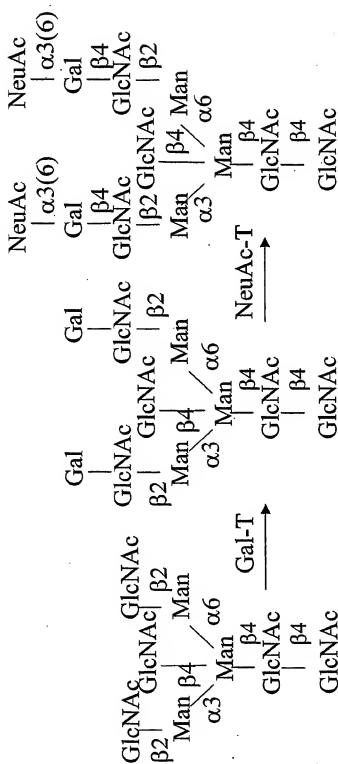


FIG. 3

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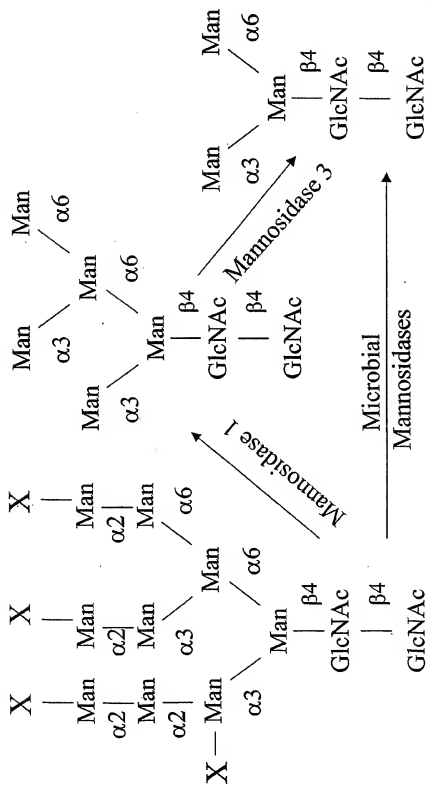


FIG. 4

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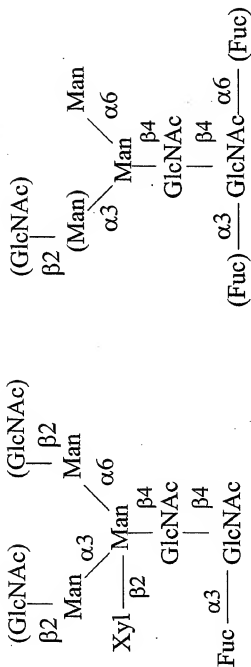
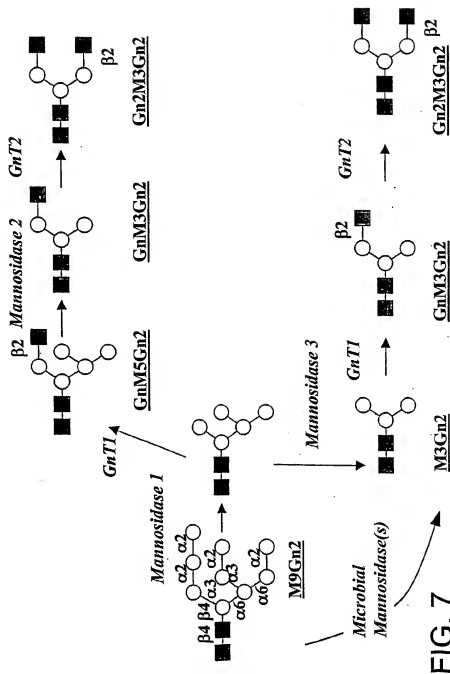


FIG. 6

FIG. 5

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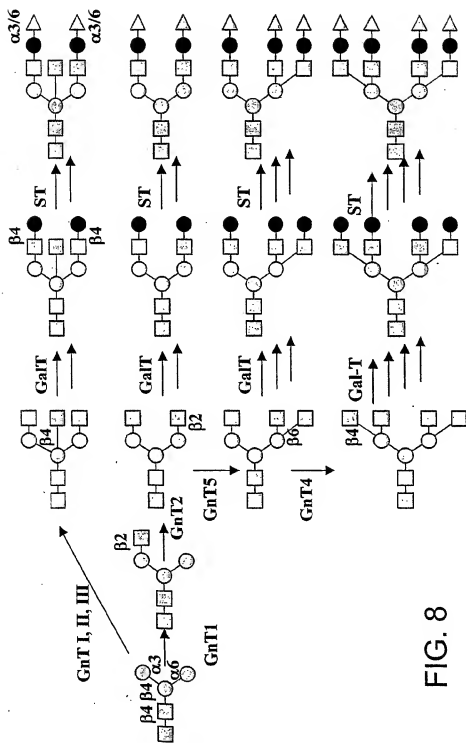


FIG. 8

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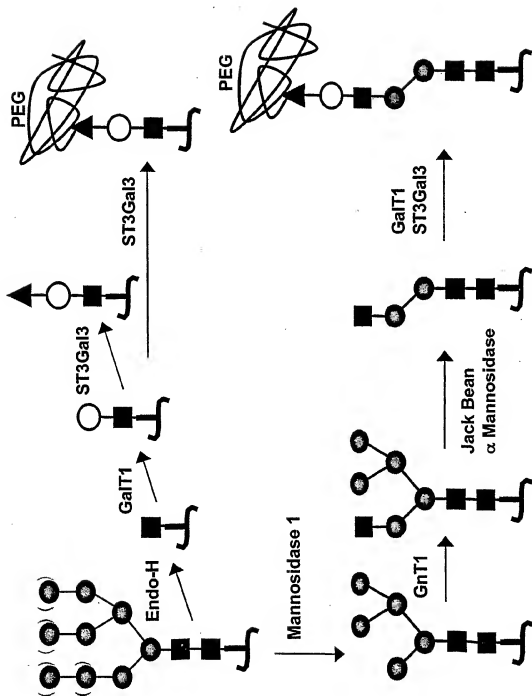


FIG. 9

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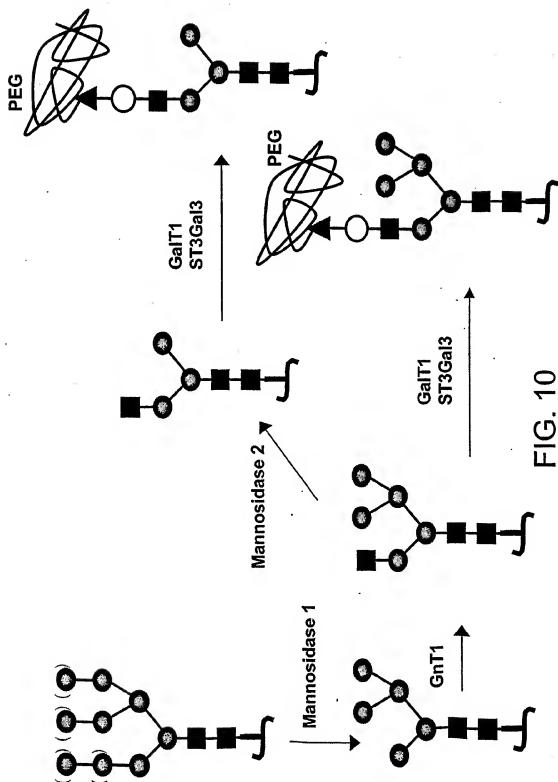


FIG. 10

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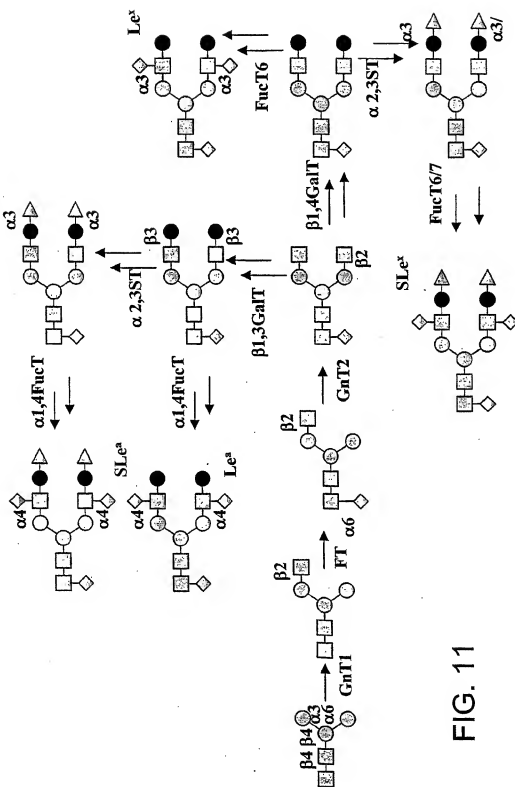


FIG. 11

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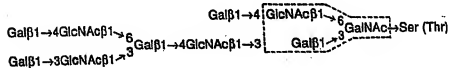
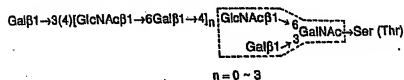
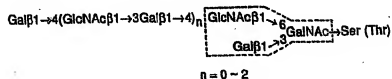
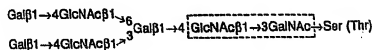
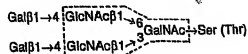
Core 1**Core 2****Core 3****Core 4**

FIG. 13

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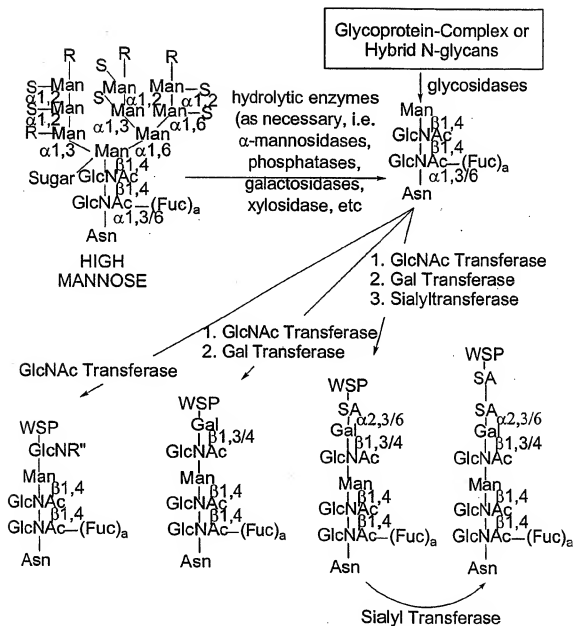


FIG. 15

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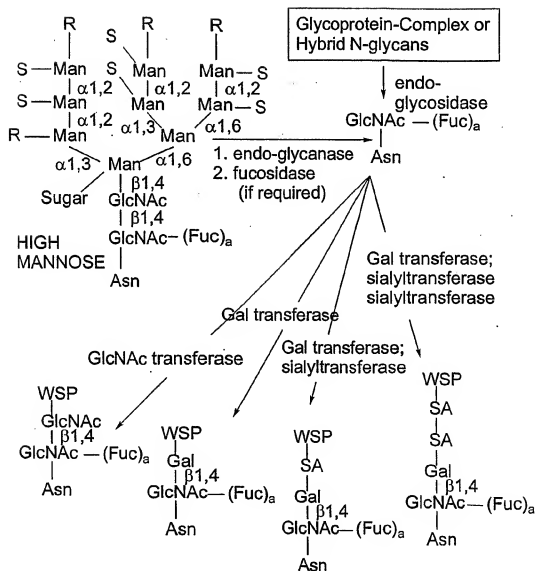


FIG. 17

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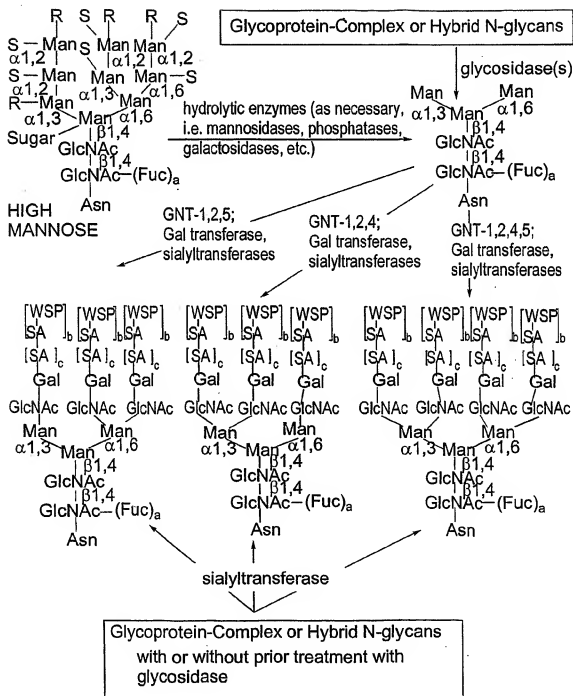


FIG. 20

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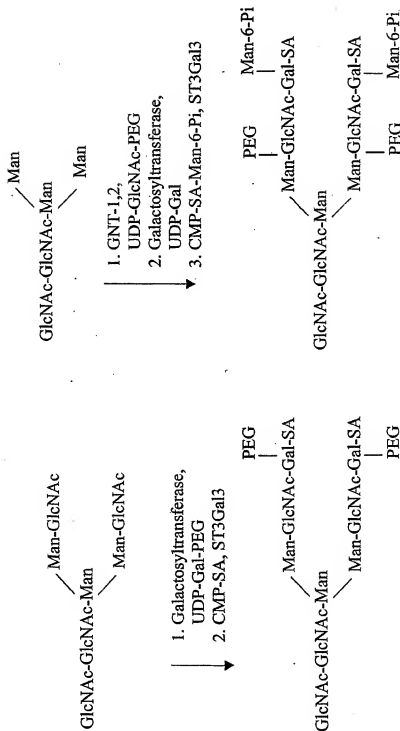


FIG. 23B

FIG. 23A

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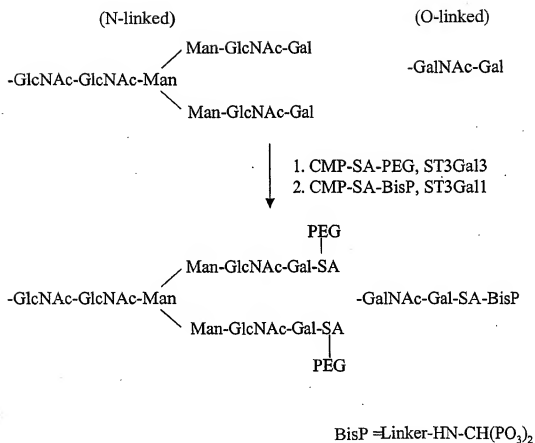


FIG. 23C

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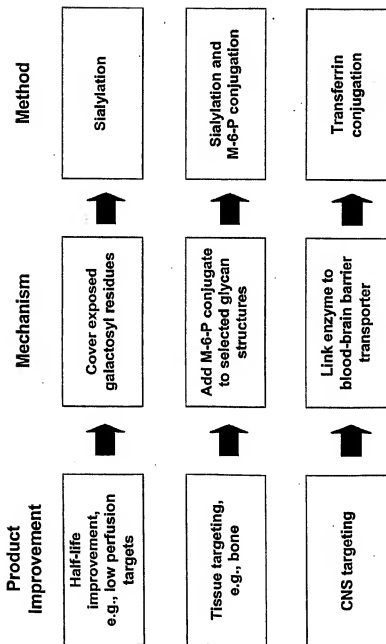


FIG. 24

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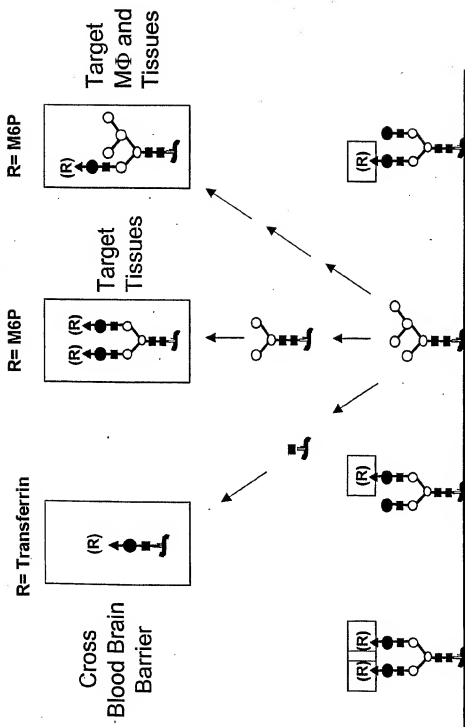


FIG. 25

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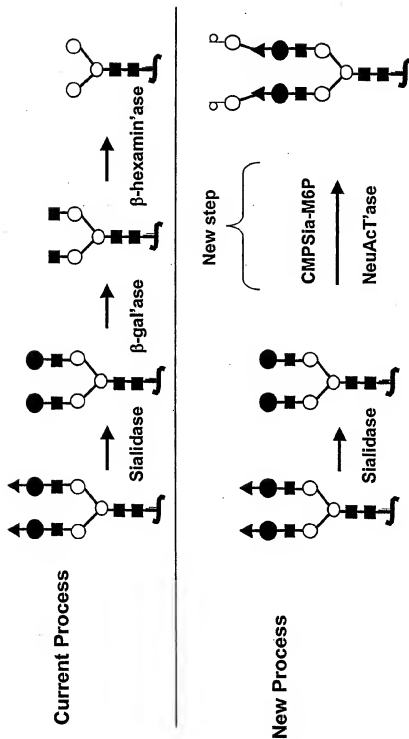


FIG. 26

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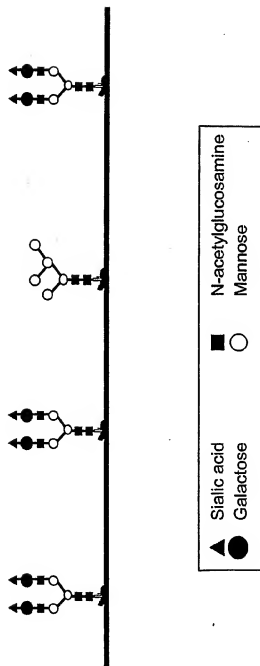


FIG. 27

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12AP1/E5 -- Viventia Biotech
 1964 -- Aventis
 20K growth hormone -- AMUR
 28P6/E6 -- Viventia Biotech
 3-Hydroxyphthaloyl-beta-lactoglobulin --
 4-IBB ligand gene therapy --
 64-Cu MAb conjugate TETA-1A3 --
 Mallinckrodt Institute of Radiology
 64-Cu MAb conjugate TETA-cT84.66
 64-Cu Trastuzumab TETA conjugate --
 Genentech
 A 200 -- Amgen
 A10255 -- Eli Lilly
 A1PDX -- Hedral Therapeutics
 A6 -- Angstrom
 aaAT-III -- Genzyme
 Abciximab -- Centocor
 ABI.001 -- Atlantic BioPharmaceuticals
 ABT-828 -- Abbott
 Accutin
 Actinohivin
 activin -- Biotech Australia, Human
 Therapeutics, Curis
 AD 439 -- Tanox
 AD 519 -- Tanox
 Adalimumab -- Cambridge Antibody Tech.
 Adenocarcinoma vaccine -- Biomira -- NIS
 Adenosine deaminase -- Enzond
 Adenosine A2B receptor antagonists --
 Adenosine Therapeutics
 ADP-001 -- Axis Genetics
 AF 13948 -- Affymax
 Afelimomab -- Knoll
 AFP-SCAN -- Immunomedics
 AG 2195 -- Corixa
 agalsidase alfa -- Transkaryotic Therapies
 agalsidase beta -- Genzyme
 AGENT-- Antisoma
 AI 300 -- Autolimmune
 AI-101 -- Teva
 AI-102 -- Teva
 AI-201 -- Autolimmune
 AI-301 -- Autolimmune
 AIDS vaccine -- ANRS, CIBG, Heseid
 Biomed, Hollis-Eden, Rome, United
 Biomedical, American Home Products,
 Maxygen
 airway receptor ligand -- IC Innovations
 AJW 2 -- Ajinomoto
 AK 30 NGF -- Alkermes
 Albuferon -- Human Genome Sciences
 albumin -- Biogen, DSM Anti-Infectives,
 Genzyme Transgenics, PPL Therapeutics,
 TranXenoGen, Welfide Corp.
 aldesleukin -- Chiron
 alefacept -- Biogen
 Alemtuzumab
 Allergy therapy -- ALK-Abello/Maxygen,
 ALK-Abello/RP Scherer
 allergy vaccines -- Allergy Therapeutics
 Alnidofibatide -- Aventis Pasteur
 Alnorine -- SRC VB VECTOR
 ALP 242 -- Gruenenthal
 Alpha antitrypsin -- Arriva/Hyland
 Immuno/ProMetic/Protease Sciences
 Alpha-1 antitrypsin -- Cutter, Bayer, PPL
 Therapeutics, Profile, ZymoGenetics,
 Arriva
 Alpha-1 protease inhibitor -- Genzyme
 Transgenics, Welfide Corp.
 Alpha-galactose fusion protein --
 Immunomedics
 Alpha-galactosidase A -- Research
 Corporation Technologies, Genzyme
 Alpha-glucosidase -- Genzyme, Novazyme
 Alpha-lactalbumin
 Alpha-L-iduronidase -- Transkaryotic
 Therapies, BioMarin
 alteplase -- Genentech
 alvircept sudotox -- NIH
 ALX-0600, a GLP-2 agonist -- NPS Allelix
 Corp.

FIG. 28A

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ALX1-11 --sNPS Pharmaceuticals
 Alzheimer's disease gene therapy
 AM-133 -- AMRAD
 Amb a 1 immunostim conj. -- Dynavax
 AMD 3100 -- AnorMED -- NIS
 AMD 3465 -- AnorMED -- NIS
 AMD 3465 -- AnorMED -- NIS
 AMD Fab -- Genentech
 Amediplase -- Menarini, Novartis
 AM-F9
 Amoebiasis vaccine
 Amphiregulin -- Octagene
 anakinra -- Amgen
 analgesic -- Nobex
 aneastim -- Amgen
 Anergix.RA -- Corixa, Organon
 Angiocidin -- InKine
 angiogenesis inhibitors -- ILEX
 AngioMab -- Antisoma
 Angiopoietins -- Regeneron/Procter &
 Gamble
 angiostatin -- EntreMed
 Angiostatin/endostatin gene therapy --
 Genetix Pharmaceuticals
 angiotensin-II, topical -- Maret
 Anthrax -- EliSys Therapeutics/US Army
 Medical Research Institute
 Anthrax vaccine
 Anti platelet-derived growth factor D human
 monoclonal antibodies -- CuraGen
 Anti-17-1A Mab 3622W94 --
 GlaxoSmithKline
 Anti-2C4 Mab -- Genentech
 anti-4-1BB monoclonal antibodies -- Bristol-
 Myers Squibb
 Anti-Adhesion Platform Tech. -- CytoVax
 Anti-adipocyte Mab -- Cambridge Antibody
 Tech./ObeSys
 antiallergics -- Maxygen
 antiallergy vaccine -- Acambis
 Anti-alpha-4-integrin Mab
 Anti-alphavβ3 integrin Mab -- Applied
 Molecular Evolution
 Anti-angiogenesis monoclonal antibodies --
 KS Biomedix/Schering AG
 Anti-B4 Mab-DC1 conjugate -- ImmunoGen
 Anti-B7 antibody PRIMATIZED -- IDEC
 Anti-B7-1 Mab 16-10A1
 Anti-B7-1 Mab 1G10
 Anti-B7-2 Mab GL-1
 Anti-B7-2-gelonin immunotoxin --
 Antibacterials/antifungals --
 Diversa/IntraBiotics
 Anti-beta-amyloid monoclonal antibodies --
 Cambridge Antibody Tech., Wyeth-Ayerst
 Anti-BLyS antibodies -- Cambridge
 Antibody Tech./Human Genome Sciences
 Antibody-drug conjugates -- Seattle
 Genetics/Eos
 Anti-C5 Mab BB5-1 -- Alexion
 Anti-C5 Mab N19-8 -- Alexion
 Anti-C8 Mab
 anticancer cytokines -- BioPulse
 anticancer matrix -- Telios Integra
 Anticancer monoclonal antibodies -- ARIUS,
 Immunex
 anticancer peptides -- Maxygen, Micrologix
 Anticancer prodrug Tech. -- Alexion
 Antibody Technologies
 anticancer Troy-Bodies -- Affite -- Affitech
 anticancer vaccine -- NIH
 anticancers -- Epimmune
 Anti-CCR5/CXCR4 sheep Mab -- KS
 Biomedix Holdings
 Anti-CD11a Mab KBA --
 Anti-CD11a Mab M17
 Anti-CD11a Mab TA-3 --
 Anti-CD11a Mab WT.1 --
 Anti-CD11b Mab -- Pharmacia
 Anti-CD11b Mab LM2
 Anti-CD154 Mab -- Biogen
 Anti-CD16-anti-CD30 Mab -- Biotest

FIG. 28B

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Anti-CD18 MAb -- Pharmacia	Anti-CD4 MAb -- Centocor, IDEC
Anti-CD19 MAb B43 --	Pharmaceuticals, Xenova Group
Anti-CD19 MAb -liposomal sodium butyrate conjugate --	Anti-CD4 MAb 16H5
Anti-CD147	Anti-CD4 MAb 4162W94 -- GlaxoSmithKline
Anti-CD19 MAb-saporin conjugate --	Anti-CD4 MAb B-F5 -- Diaclone
Anti-CD19-dsFv-PE38-immunotoxin --	Anti-CD4 MAb GK1-5
Anti-CD2 MAb 12-15 --	Anti-CD4 MAb KT6
Anti-CD2 MAb B-E2 -- Diaclone	Anti-CD4 MAb OX38
Anti-CD2 MAb OX34 --	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb OX54 --	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX55 --	Anti-CD4 MAb W3/25
Anti-CD2 MAb RM2-1	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb RM2-2	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-4	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD20 MAb BCA B20	Anti-CD40 MAb
Anti-CD20-anti-Fc alpha RI bispecific MAb -- Medarex, Tenovus	Anti-CD40 MAb 5D12 -- Tanox
Anti-CD22 MAb-saporin-6 complex --	Anti-CD44 MAb A3D8
Anti-CD3 Immunotoxin --	Anti-CD44 MAb GKWA3
Anti-CD3 MAb 145-2C11 -- Pharming	Anti-CD44 MAb IM7
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD44 MAb KM81
Anti-CD3 MAb humanised -- Protein Design, RW Johnson	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb WT32	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb-ricin-chain-A conjugate --	Anti-CD45RB MAb
Anti-CD3 MAb-xanthine-oxidase conjugate --	Anti-CD48 MAb HuLy-m3
Anti-CD30 MAb BerH2 -- Medac	Anti-CD48 MAb WM-63
Anti-CD30 MAb-saporin conjugate	Anti-CD5 MAb -- Becton Dickinson
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD5 MAb OX19
Anti-CD38 MAb AT13/5	Anti-CD6 MAb
Anti-CD38 MAb-saporin conjugate	Anti-CD7 MAb-PAP conjugate
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb -- Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD8 MAb OX8
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD4 idiotype vaccine	Anti-CD80 MAb P7C10 -- ID Vaccine
	Anti-CD8-idarubicin conjugate
	Anti-CEA MAb CE-25
	Anti-CEA MAb MN 14 -- Immunomedics

FIG. 28C

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- Anti-CEA MAb MN14-PE40 conjugate -- Immunomedics
- Anti-CEA MAb T84.66-interleukin-2 conjugate
- Anti-CEA sheep MAb -- KS Biomedix Holdings
- Anti-cell surface monoclonal antibodies -- Cambridge Antibody Tech. /Pharmacia
- Anti-c-erbB2-anti-CD3 bifunctional MAb -- Otsuka
- Anti-CMV MAb -- Scotgen
- Anti-complement
- Anti-CTLA-4 MAb
- Anti-EGFR catalytic antibody -- Hersed Biomed
- anti-EGFR immunotoxin -- IVAX
- Anti-EGFR MAb -- Abgenix
- Anti-EGFR MAb 528
- Anti-EGFR MAb KSB 107 -- KS Biomedix
- Anti-EGFR MAb-DM1 conjugate -- ImmunoGen
- Anti-EGFR MAb-LA1 --
- Anti-EGFR sheep MAb -- KS Biomedix
- Anti-FAP MAb F19-I-131
- Anti-Fas IgM MAb CH11
- Anti-Fas MAb Jo2
- Anti-Fas MAb RK-8
- Anti-Fit-1 monoclonal antibodies -- ImClone
- Anti-fungal peptides -- State University of New York
- antifungal tripeptides -- BTG
- Anti-ganglioside GD2 antibody-interleukin-2 fusion protein -- Lexigen
- Anti-GM2 MAb -- Kyowa
- Anti-GM-CSF receptor monoclonal antibodies -- AMRAD
- Anti-gp130 MAb -- Tosoh
- Anti-HCA monoclonal antibodies -- AltaRex/Epigen
- Anti-hCG antibodies -- Abgenix/AVI BioPharma
- Anti-heparanase human monoclonal antibodies -- Oxford Glycosciences/Medarex
- Anti-hepatitis C virus human monoclonal antibodies -- XTL Biopharmaceuticals
- Anti-HER-2 antibody gene therapy
- Anti-herpes antibody -- Epicyte
- Anti-HIV antibody -- Epicyte
- anti-HIV catalytic antibody -- Hersed Biomed
- anti-HIV fusion protein -- Idun
- anti-HIV proteins -- Cangene
- Anti-HM1-24 MAb -- Chugai
- Anti-hrR3 MAb
- Anti-Human-Carcinoma-Antigen MAb -- Epicyte
- Anti-ICAM-1 MAb -- Boehringer Ingelheim
- Anti-ICAM-1 MAb 1A-29 -- Pharmacia
- Anti-ICAM-1 MAb HA58
- Anti-ICAM-1 MAb YN1/1.7.4
- Anti-ICAM-3 MAb ICM3 -- ICOS
- Anti-idiotypic breast cancer vaccine 11D10
- Anti-idiotypic breast cancer vaccine ACA14C5 --
- Anti-idiotypic cancer vaccine -- ImClone Systems/Merck KGaA ImClone, Viventia Biotech
- Anti-idiotypic cancer vaccine 1A7 -- Titan
- Anti-idiotypic cancer vaccine 3H1 -- Titan
- Anti-idiotypic cancer vaccine TriAb -- Titan
- Anti-idiotypic Chlamydia trachomatis vaccine
- Anti-idiotypic colorectal cancer vaccine -- Novartis
- Anti-idiotypic colorectal cancer vaccine -- Onyvox
- Anti-idiotypic melanoma vaccine -- IDEC Pharmaceuticals
- Anti-idiotypic ovarian cancer vaccine ACA 125
- Anti-idiotypic ovarian cancer vaccine AR54 - AltaRex

FIG. 28D

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- Anti-idiotype ovarian cancer vaccine CA-125 – AltaRex, Biomira
- Anti-IgE catalytic antibody – Hesed Biomed
- Anti-IgE MAb E26 – Genentech
- Anti-IGF-1 MAb
- anti-inflammatory – GeneMax
- anti-inflammatory peptide – BTG
- anti-integrin peptides – Burnha
- Anti-interferon-alpha-receptor MAb 64G12 – Pharma Pacific Management
- Anti-interferon-gamma MAb – Protein Design Labs
- Anti-interferon-gamma polyclonal antibody – Advanced Biotherapy
- Anti-interleukin-10 MAb –
- Anti-interleukin-12 MAb –
- Anti-interleukin-1-beta polyclonal antibody – R&D Systems
- Anti-interleukin-2 receptor MAb 2A3
- Anti-interleukin-2 receptor MAb 33B3-1 – Immunotech
- Anti-interleukin-2 receptor MAb ART-18
- Anti-interleukin-2 receptor MAb LO-Tact-1
- Anti-interleukin-2 receptor MAb Mikbeta1
- Anti-interleukin-2 receptor MAb NDS61
- Anti-interleukin-4 MAb 11B11
- Anti-interleukin-5 MAb – Wallace Laboratories
- Anti-interleukin-6 MAb – Centocor, Diacorne, Pharmadigm
- Anti-interleukin-8 MAb – Abgenix
- Anti-interleukin-8 MAb – Xenotech
- Anti-JL1 MAb
- Anti-Klebsiella sheep MAb – KS Biomedix Holdings
- Anti-Laminin receptor MAb-liposomal doxorubicin conjugate
- Anti-LCG MAb – Cytoclonal
- Anti-lipopolysaccharide MAb – VitaResc
- Anti-L-selectin monoclonal antibodies – Protein Design Labs, Abgenix, Stanford University
- Anti-MBL monoclonal antibodies – Alexion/Brigham and Women's Hospital
- Anti-MHC monoclonal antibodies
- Anti-MIF antibody humanised – IDEC, Cytokine PharmaSciences
- Anti-MRSA/VRSA sheep MAb – KS Biomedix Holdings
- Anti-mu MAb – Novartis
- Anti-MUC-1 MAb
- Anti-MUC 18
- Anti-Nogo-A MAb IN1
- Anti-nuclear autoantibodies – Procyon
- Anti-ovarian cancer monoclonal antibodies – Dompe
- Anti-p185 monoclonal antibodies
- Anti-p43 MAb
- Antiparasitic vaccines
- Anti-PDGF/bFGF sheep MAb – KS Biomedix
- Anti-properdin monoclonal antibodies – Abgenix/Gliatech
- Anti-PSMA (prostate specific membrane antigen)
- Anti-PSMA MAb J591 – BZL Biologics
- Anti-Rev MAb gene therapy –
- Anti-RSV antibodies – Epicyte, Intracell
- Anti-RSV monoclonal antibodies – Medarex/MedImmune, Applied Molecular Evolution/MedImmune
- Anti-RSV MAb, inhalation – Alkermes/MedImmune
- Anti-RT gene therapy
- Antisense K-ras RNA gene therapy
- Anti-SF-25 MAb
- Anti-sperm antibody – Epicyte
- Anti-Tac(Fv)-PE38 conjugate
- Anti-TAPA/CD81 MAb AMP1
- Anti-tat gene therapy

FIG. 28E

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Anti-TCR-alphabeta MAb H57-597
 Anti-TCR-alphabeta MAb R73
 Anti-tenascin MAb BC-4-I-131
 Anti-TGF-beta human monoclonal
 antibodies -- Cambridge Antibody Tech.,
 Genzyme
 Anti-TGF-beta MAb 2G7 -- Genentech
 Antithrombin III -- Genzyme Transgenics,
 Aventis, Bayer, Behringwerke, CSL,
 Myriad
 Anti-Thy1 MAb
 Anti-Thy1.1 MAb
 Anti-tissue factor/factor VIIA sheep MAb --
 KS Biomedix
 Anti-TNF monoclonal antibodies --
 Centocor, Chiron, Peptech, Pharacia,
 Sero
 Anti-TNF sheep MAb -- KS Biomedix
 Holdings
 Anti-TNFalpha MAb -- Genzyme
 Anti-TNFalpha MAb B-C7 -- Diaclone
 Anti-tooth decay MAb -- Planet BioTech.
 Anti-TRAIL receptor-1 MAb -- Takeda
 Antitumour RNases -- NIH
 Anti-VCAM MAb 2A2 -- Alexion
 Anti-VCAM MAb 3F4 -- Alexion
 Anti-VCAM-1 MAb
 Anti-VEC MAb -- ImClone
 Anti-VEGF MAb -- Genentech
 Anti-VEGF MAb 2C3
 Anti-VEGF sheep MAb -- KS Biomedix
 Holdings
 Anti-VLA-4 MAb HP1/2 -- Biogen
 Anti-VLA-4 MAb PS/2
 Anti-VLA-4 MAb R1-2
 Anti-VLA-4 MAb TA-2
 Anti-VAP-1 human MAb
 Anti-VRE sheep MAb -- KS Biomedix
 Holdings
 ANUP -- TranXenoGen
 ANUP-1 -- Pharis

AOP-RANTES -- Senetek
 Apan-CH -- Praecis Pharmaceuticals
 APC-8024 -- Demegen
 ApoA-1 -- Milano, Pharmacia
 Apogen -- Alexion
 apolipoprotein A1 -- Avanir
 Apolipoprotein E -- Bio-Tech. General
 Applaggin -- Biogen
 aprotinin -- ProdiGene
 APT-070C -- AdProTech
 AR 177 -- Aronex Pharmaceuticals
 AR 209 -- Aronex Pharmaceuticals,
 Antigenics
 AR545C
 ARGENT gene delivery systems -- ARIAD
 Arresten
 ART-123 -- Asahi Kasei
 arylsulfatase B -- BioMarin
 Arylsulfatase B, Recombinant human --
 BioMarin
 AS 1051 -- Ajinomoto
 ASI-BCL -- Intracell
 Asparaginase - Merck
 ATL-101 -- Alizyme
 Atrial natriuretic peptide -- Pharis
 Aurintricarboxylic acid-high molecular
 weight
 Autoimmune disorders -- GPC
 Biotech/MorphoSys
 Autoimmune disorders and transplant
 rejection -- Bristol-Myers Squibb/Genzyme
 Tra
 Autoimmune disorders/cancer --
 Abgenix/Chiron, CuraGen
 Autotaxin
 Avicidin -- NeoRx
 axogenesis factor-1 -- Boston Life Sciences
 Axokine -- Regeneron
 B cell lymphoma vaccine -- Biomira
 B7-1 gene therapy --
 BABS proteins -- Chiron

FIG. 28F

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BAM-002 -- Novelos Therapeutics
 Basiliximab (anti CD25 MAb) -- Novartis
 Bay-16-9996 -- Bayer
 Bay-39-9437 -- Bayer
 Bay-50-4798 -- Bayer
 BB-10153 -- British Biotech
 BBT-001 -- Bolder BioTech.
 BBT-002 -- Bolder BioTech.
 BBT-003 -- Bolder BioTech.
 BBT-004 -- Bolder BioTech.
 BBT-005 -- Bolder BioTech.
 BBT-006 -- Bolder BioTech.
 BBT-007 -- Bolder BioTech.
 BCH-2763 -- Shire
 BCSF -- Millenium Biologix
 BDNF -- Regeneron -- Amgen
 Becapiermin -- Johnson & Johnson, Chiron
 Bectumomab -- Immunomedics
 Beriplast -- Aventis
 Beta-adrenergic receptor gene therapy --
 University of Arkansas
 bFGF -- Scios
 BI 51013 -- Behringwerke AG
 BIBH 1 -- Boehringer Ingelheim
 BIM-23190 -- Beaufour-Ipsen
 birch pollen immunotherapy -- Pharmacia
 bispecific fusion proteins -- NIH
 Bispecific MAb 2B1 -- Chiron
 Bitistatin
 BIWA 4 -- Boehringer Ingelheim
 blood substitute -- Northfield, Baxter Intl.
 BLP-25 -- Biomira
 BLS-0597 -- Boston Life Sciences
 BLyS -- Human Genome Sciences
 BLyS radiolabelled -- Human Genome
 Sciences
 BM 06021 -- Boehringer Mannheim
 BM-202 -- BioMarin
 BM-301 -- BioMarin
 BM-301 -- BioMarin
 BM-302 -- BioMarin
 BMP 2 -- Genetics Institute/Medtronic-
 Sofamor Danek, Genetics Institute/
 Collagenesis, Genetics
 Institute/Yamanouch
 BMP 2 gene therapy
 BMP 52 -- Aventis Pasteur, Biopharm
 BMP-2 -- Genetics Institute
 BMS 182248 -- Bristol-Myers Squibb
 BMS 202448 -- Bristol-Myers Squibb
 bone growth factors -- IsoTis
 BPC-15 -- Pfizer
 brain natriuretic peptide --
 Breast cancer -- Oxford
 GlycoSciences/Medarex
 Breast cancer vaccine -- Therion Biologics,
 Oregon
 BSSL -- PPL Therapeutics
 BST-2001 -- BioStratum
 BST-3002 -- BioStratum
 BTI 322 --
 butyrylcholinesterase -- Shire
 C 6822 -- COR Therapeutics
 C1 esterase inhibitor -- Pharming
 C3d adjuvant -- AdProTech
 CAB-2.1 -- Millennium
 calcitonin -- Inhale Therapeutics Systems,
 Aventis, Genetronics, TranXenoGen,
 Unigene, Rhone Poulenc Rohrer
 calcitonin -- oral -- Nobex, Emisphere,
 Pharmaceutical Discovery
 Calcitonin gene-related peptide -- Asahi
 Kasei -- Unigene
 calcitonin, human -- Suntory
 calcitonin, nasal -- Novartis, Unigene
 calcitonin, Panoderm -- Elan
 calcitonin, Peptitrol -- Shire
 calcitonin, salmon -- Therapicon
 calin -- Biopharm
 Calphobindin I
 calphobindin I -- Kowa
 calreticulin -- NYU

FIG. 28G

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Campath-1G
 Campath-1M
 cancer therapy -- Cangene
 cancer vaccine -- Aixlie, Aventis Pasteur,
 Center of Molecular Immunology, YM
 BioSciences, Cytos, Genzyme,
 Transgenics, GlobelImmune, Igeneon,
 ImClone, Virogenetics, InterCell, Iomai,
 Jenner Biotherapies, Memorial Sloan-
 Kettering Cancer Center, Sydney Kimmel
 Cancer Center, Novavax, Protein
 Sciences, Argonex, SIGA
 Cancer vaccine ALVAC-CEA B7.1 --
 Aventis Pasteur/Therion Biologics
 Cancer vaccine CEA-TRICOM -- Aventis
 Pasteur/Therion Biologics
 Cancer vaccine gene therapy -- Cantab
 Pharmaceuticals
 Cancer vaccine HER-2/neu -- Corixa
 Cancer vaccine THERATOPE -- Biomira
 cancer vaccine, PolyMASC -- Valentis
 Candida vaccine -- Corixa, Inhibitex
 Canstatin -- ILEX
 CAP-18 -- Panorama
 Cardiovascular gene therapy -- Collateral
 Therapeutics
 carperitide -- Suntory
 Casocidin-1 -- Pharis
 CAT 152 -- Cambridge Antibody Tech.
 CAT 192 -- Cambridge Antibody Tech.
 CAT 213 -- Cambridge Antibody Tech.
 Catalase-- Enzon
 Cat-PAD -- Circassia
 CB 0006 -- Celltech
 CCK(27-32)-- Akzo Nobel
 CCR2-64I -- NIH
 CD, Procept -- Paligent
 CD154 gene therapy
 CD39 -- Immunex
 CD39-L2 -- Hyseq
 CD39-L4 -- Hyseq
 CD4 fusion toxin -- Senetek
 CD4 IgG -- Genentech
 CD4 receptor antagonists --
 Pharmacocepeia/Progenics
 CD4 soluble -- Progenics
 CD4, soluble -- Genzyme Transgenics
 CD40 ligand -- Immunex
 CD4-ricin chain A -- Genentech
 CD59 gene therapy -- Alexion
 CD8 TIL cell therapy -- Aventis Pasteur
 CD8, soluble -- Avidex
 CD95 ligand -- Roche
 CDP 571 -- Celltech
 CDP 850 -- Celltech
 CDP-860 (PEG-PDGF MAb) -- Celltech
 CDP 870 -- Celltech
 CDS-1 -- Ernest Orlando
 Cedelizumab -- Ortho-McNeil
 Cetermin -- Insmed
 CETP vaccine -- Avant
 Cetorelix
 Cetuximab
 CGH 400 -- Novartis
 CGP 42934 -- Novartis
 CGP 51901 -- Tanox
 CGRP -- Unigene
 CGS 27913 -- Novartis
 CGS 32359 -- Novartis
 Chagas disease vaccine -- Corixa
 chemokines -- Immune Response
 CHH 380 -- Novartis
 chitinase -- Genzyme, ICOS
 Chlamydia pneumoniae vaccine -- Antex
 Biologics
 Chlamydia trachomatis vaccine -- Antex
 Biologics
 Chlamydia vaccine -- GlaxoSmithKline
 Cholera vaccine CVD 103-HgR -- Swiss
 Serum and Vaccine Institute Berne
 Cholera vaccine CVD 112 -- Swiss Serum
 and Vaccine Institute Berne

FIG. 28H

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Cholera vaccine inactivated oral -- SBL	CRL 1605 -- CytRx
Vaccin	CS-560 -- Sankyo
Chrysalin -- Chrysalis BioTech.	CSF -- ZymoGenetics
CI-782 -- Hitachi Kase	CSF-G -- Hangzhou, Dong-A, Hanmi
Ciliary neurotrophic factor -- Fidia, Roche	CSF-GM -- Cangene, Hunan, LG Chem
CIM project -- Active Biotech	CSF-M -- Zarix
CL 329753 -- Wyeth-Ayerst	CT 1579 -- Merck Frosst
CL22, Cobra -- ML Laboratories	CT 1786 -- Merck Frosst
Clenoliximab -- IDEC	CT-112 ^A -- BTG
Clostridium difficile antibodies -- Epicycle	CTB-134L -- Xenova
clotting factors -- Octagene	CTC-111 -- Kaketsuken
CMB 401 -- Celltech	CTGF -- FibroGen
CNTF -- Sigma-Tau	CTLA4-Ig -- Bristol-Myers Squibb
Cocaine abuse vaccine -- Cantab,	CTLA4-Ig gene therapy --
ImmuLogic, Scripps	CTP-37 -- AVI BioPharma
coccidiomycosis vaccine -- Arizo	C-type natriuretic peptide -- Suntory
collagen -- Type I -- Pharming	CVS 995 -- Corvas Intl.
Collagen formation inhibitors -- FibroGen	CX 397 -- Nikko Kyodo
Collagen/hydroxyapatite/bone growth factor	CY 1747 -- Epimmune
-- Aventis Pasteur, Biopharm, Orquest	CY 1748 -- Epimmune
collagenase -- BioSpecifics	Cyanovirin-N
Colorectal cancer vaccine -- Wistar Institute	Cystic fibrosis therapy -- CBR/IVAX
Component B, Recombinant -- Sero	CYT 351
Connective tissue growth factor inhibitors --	cytokine Traps -- Regeneron
FibroGen/Taisho	cytokines -- Enzon, Cytodonal
Contortrostatin	Cytomegalovirus glycoprotein vaccine --
contraceptive vaccine -- Zonagen	Chiron, Aquila Biopharmaceuticals,
Contraceptive vaccine hCG	Aventis Pasteur, Virogenetics
Contraceptive vaccine male reversible --	Cytomegalovirus vaccine live -- Aventis
IMMUCON	Pasteur
Contraceptive vaccine zona pellucida --	Cytosine deaminase gene therapy --
Zonagen	GlaxoSmithKline
Copper-64 labelled Mab TETA-1A3 -- NCI	DA-3003 -- Dong-A
Coralyne	DAB389interleukin-6 -- Senetek
Corsevin M	DAB389interleukin-7
C-peptide analogues -- Schwarz	DAC:GLP-2 -- ConjuChem, Inc.
CPI-1500 -- Consensus	Daclizumab (anti-IL2R Mab) -- Protein
CRF -- Neurobiological Tech.	Design Labs
cRGDfV pentapeptide --	DAMP ^A -- Incyte Genomics
CRL 1095 -- CytRx	Daniplestim -- Pharmacia
CRL 1336 -- CytRx	darbepoetin alfa -- Amgen

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DBI-3019 -- Diabetogen
 DCC -- Genzyme
 DDF -- Hyseq
 decorin -- Integra, Telios
 defensins -- Large Scale Biology
 DEGR-VIIa
 Delimmunised antibody 3B6/22 AGEN
 Deimmunised anti-cancer antibodies --
 Biovation/Viragen
 Dendroamide A
 Dengue vaccine -- Bavarian Nordic, Merck
 denileukin diftotox -- Ligand
 DES-1101 -- Desmos
 desirudin -- Novartis
 desmopressin -- Unigene
 Desmoteplase -- Merck, Schering AG
 Destablase
 Diabetes gene therapy -- DeveloGen, Pfizer
 Diabetes therapy -- Crucell
 Diabetes type 1 vaccine -- Diamyd
 Therapeutics
 DiaCIM -- YM BioSciences
 dialytic oligopeptides -- Research Corp
 Diamyd -- Diamyd Therapeutics
 DiaPep227 -- Peppen
 DiavaX -- Corixa
 Digoxin MAb -- Glaxo
 Diphtheria tetanus pertussis-hepatitis B
 vaccine -- GlaxoSmithKline
 DIR therapy -- Solis Therapeutics --
 DNase -- Genentech
 Dornase alfa -- Genentech
 Dornase alfa, inhalation -- Genentech
 Doxorubicin-anti-CEA MAb conjugate --
 Immunomedics
 DP-107 -- Trimeris
 drotrecogin alfa -- Eli Lilly
 DTctGMCSF
 DTP-polio vaccine -- Aventis Pasteur
 DU 257-KM231 antibody conjugate --
 Kyowa
 dural graft matrix -- Integra
 Duteplase -- Baxter Intl.
 DWP-401 -- Daewoong
 DWP-404 -- Daewoong
 DWP-408 -- Daewoong
 Dx 88 (Epi-KAL2) -- Dyax
 Dx 890 (elastin inhibitors) -- Dyax
 E coli O157 vaccine -- NIH
 E21-R -- BresaGen
 Eastern equine encephalitis virus vaccine --
 Echicetin --
 Echinhibin 1 --
 Echistatin -- Merck
 Echitamine --
 Ecromeximab -- Kyowa Hakko
 EC-SOD -- PPL Therapeutics
 Eculizumab (5G1.1) -- Alexion
 EDF -- Ajinomoto
 EDN derivative -- NIH
 EDNA -- NIH
 Edobacomab -- XOMA
 Edrecolomab -- Centocor
 EF 5077
 Efalizumab -- Genentech
 EGF fusion toxin -- Seragen, Ligand
 EGF-P64k vaccine -- Center of Molecular
 Immunology
 EL 246 -- LigoCyte
 elastase inhibitor -- Synergen
 elcatonin -- Therapicon
 EMD 72000 -- Merck KGaA
 Emdogain -- BIORA
 emfilermin -- AMRAD
 Emoctakin -- Novartis
 enamel matrix protein -- BIORA
 Endo III -- NYU
 endostatin -- EntreMed, Pharis
 Enhancins -- Micrologix
 Enlimomab -- Isis Pharm.
 Enoxaparin sodium -- Phamuka

FIG. 28J

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enzyme linked antibody nutrient depletion
 therapy -- KS Biomedix Holdings
 Eosinophil-derived neutralizing agent --
 EP-51216 -- Asta Medica
 EP-51389 -- Asta Medica
 EPH family ligands -- Regeneron
 Epidermal growth factor -- Hitachi Kasei,
 Johnson & Johnson
 Epidermal growth factor fusion toxin --
 Senetek
 Epidermal growth factor-genistein --
 EPI-HNE-4 -- Dyax
 EPI-KAL2 -- Dyax
 Epoetin-alfa -- Amgen, Dragon
 Pharmaceuticals, Nanjing Huaxin
 Epratuzumab -- Immunomedics
 Epstein-Barr virus vaccine --
 Aviron/SmithKline Beecham, Bioresearch
 Eptacog alfa -- Novo Nordisk
 Eptifibatide -- COR Therapeutics
 erb-38 --
 Erlizumab -- Genentech
 erythropoietin -- Alkermes, ProLease, Dong-
 A, Elanex, Genetics Institute, LG Chem,
 Protein Sciences, Serono, Snow Brand,
 SRC VB VECTOR, Transkaryotic
 Therapies
 Erythropoietin Beta -- Hoffman La Roche
 Erythropoietin/Epoetin alfa -- Chugai
 Escherichia coli vaccine -- North American
 Vaccine, SBL Vaccin, Swiss Serum and
 Vaccine Institute Berne
 etanercept -- Immunex
 examorelin -- Mediolanum
 Exendin 4 -- Amylin
 exonuclease VII
 F 105 -- Centocor
 F-992 -- Fornix
 Factor IX -- Alpha Therapeutics, Welfide
 Corp., CSL, enetics Institute/AHP,
 Pharmacia, PPL Therapeutics
 Factor IX gene therapy -- Cell Genesys
 Factor VII -- Novo Nordisk, Bayer, Baxter
 Intl.
 Factor VIIa -- PPL Therapeutics,
 ZymoGenetics
 Factor VIII -- Bayer Genentech, Beaufour-
 Ipsen, CLB, Inex, Octagen, Pharmacia,
 Pharming
 Factor VIII -- PEGylated -- Bayer
 Factor VIII fragments -- Pharmacia
 Factor VIII gene therapy -- Targeted
 Genetics
 Factor VIII sucrose formulation -- Bayer,
 Genentech
 Factor VIII-2 -- Bayer
 Factor VIII-3 -- Bayer
 Factor Xa inhibitors -- Merck, Novo Nordisk,
 Mochida
 Factor XIII -- ZymoGenetics
 Factors VIII and IX gene therapy -- Genetics
 Institute/Targeted Genetics
 Famoxin -- Genset
 Fas (delta) TM protein -- LXR BioTech.
 Fas TR -- Human Genome Sciences
 Felvizumab -- Scotgen
 FFR-VIIa -- Novo Nordisk
 FG-001 -- F-Gene
 FG-002 -- F-Gene
 FG-004 -- F-Gene
 FG-005 -- F-Gene
 FGF + fibrin -- Repair
 Fibrimage -- Bio-Tech. General
 fibrin-binding peptides -- ISIS Innovation
 fibrinogen -- PPL Therapeutics, Pharming
 fibroblast growth factor -- Chiron, NYU,
 Ramot, ZymoGenetics
 fibrolase conjugate -- Schering AG
 Filgrastim -- Amgen
 filgrastim -- PDA modified -- Xencor
 FLT-3 ligand -- Immunex
 FN18 CRM9 --

FIG. 28K

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follistatin -- Biotech Australia, Human Therapeutics
 follitropin alfa -- Alkermes, ProLease, PowderJect, Sero, Akzo Nobel
 Follitropin Beta -- Bayer, Organon
 FP 59
 FSH -- Ferring
 FSH + LH -- Ferring
 F-spondin -- CeNeS
 fusion protein delivery system -- UAB Research Foundation
 fusion toxins -- Boston Life Sciences
 G 5598 -- Genentech
 GA-II -- Transkaryotic Therapies
 Gamma-interferon analogues -- SRC VB VECTOR
 Ganirelix -- Roche
 gastric lipase -- Meristem
 Gavilimomab --
 G-CSF -- Amgen, SRC VB VECTOR
 GDF-1 -- CeNeS
 GDF-5 -- Biopharm
 GDNF (glial derived neurotrophic factor) -- Amgen
 gelsolin -- Biogen
 Gemtuzumab ozogamicin -- Celltech
 Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies
 Glanzmann thrombasthenia gene therapy --
 Glatiramer acetate -- Yeda
 glial growth factor 2 -- CeNeS
 GLP-1 -- Amylin, Suntory, TheraTech, Watson
 GLP-1 peptide analogues -- Zealand Pharmaceuticals
 GLP-2 -- Novo Nordisk, Ontario, Inc., Suntory Limited
 glucagon -- Eli Lilly, ZymoGenetics
 Glucagon-like peptide 1-7-36 amide -- Suntory
 Glucogen-like peptide -- Amylin
 Glucocerebrosidase -- Genzyme
 glutamate decarboxylase -- Genzyme Transgenics
 Glycoprotein S3 -- Kureha
 GM-CSF -- Immuhex
 GM-CSF tumour vaccine -- PowderJect
 GnRH immunotherapeutic -- Protherics
 Goserelin (LhRH antagonist) -- AstraZeneca
 gp75 antigen -- ImClone
 gp96 -- Antigenics
 GPI 0100 -- Galenica
 GR 4991W93 -- GlaxoSmithKline
 Granulocyte colony-stimulating factor -- Dong-A
 Granulocyte colony-stimulating factor conjugate
 grass allergy therapy -- Dynavax
 GRF1-44 -- ICN
 Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo
 growth factor peptides -- Biotherapeutics
 growth hormone -- LG Chem
 growth hormone, Recombinant human -- Sero
 GT 4086 -- Gliatech
 GW 353430 -- GlaxoSmithKline
 GW-278884 -- GlaxoSmithKline
 H 11 -- Viventia Biotech
 H5N1 influenza A virus vaccine -- Protein Sciences
 haemoglobin -- Biopure
 haemoglobin 3011, Recombinant -- Baxter Healthcare
 haemoglobin crosumaril -- Baxter Intl.
 haemoglobin stabilized -- Ajinomoto
 haemoglobin, recombinant -- Apex
 HAF -- Immune Response
 Hantavirus vaccine
 HB 19
 HBNF -- Regeneron
 HCC-1 -- Pharis

FIG. 28L

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hCG -- Milkhaus
 hCG vaccine -- Zonagen
 HE-317 -- Hollis-Eden Pharmaceuticals
 Heat shock protein cancer and influenza vaccines -- StressGen
 Helicobacter pylori vaccine -- Acambis, AstraZeneca/CSL, Chiron, Provalis
 Helistat-G -- GalaGen
 Hemolink -- Hemosol
 hepapoietin -- Snow Brand
 heparanase -- InSight
 heparinase I -- Ibex
 heparinase III -- Ibex
 Hepatitis A vaccine -- American Biogenetic Sciences
 Hepatitis A vaccine inactivated
 Hepatitis A vaccine Nothav -- Chiron
 Hepatitis A-hepatitis B vaccine -- GlaxoSmithKline
 hepatitis B therapy -- Tripep
 Hepatitis B vaccine -- Amgen, Chiron SpA, Meiji Milk, NIS, Prodeva, PowderJect, Rhein Biotech
 Hepatitis B vaccine recombinant -- Evans Vaccines, Epitex Combiotech, Genentech, MedImmune, Merck Sharp & Dohme, Rhein Biotech, Shantha Biotechnics, Vector, Yeda
 Hepatitis B vaccine recombinant TGP 943 -- Takeda
 Hepatitis C vaccine -- Bavarian Nordic, Chiron, Innogenetics Acambis,
 Hepatitis D vaccine -- Chiron Vaccines
 Hepatitis E vaccine recombinant -- Genelabs/GlaxoSmithKline, Novavax
 hepatocyte growth factor -- Panorama, Sosei
 hepatocyte growth factor kringle fragments -
 - Entremed
 Her-2/Neu peptides -- Corixa
 Herpes simplex glycoprotein DNA vaccine -- Merck, Wyeth-Lederle Vaccines-Malvern, Genentech, GlaxoSmithKline, Chiron, Takeda
 Herpes simplex vaccine -- Cantab Pharmaceuticals, CEL-SCI, Henderson Morley
 Herpes simplex vaccine live -- ImClone Systems/Wyeth-Lederle, Aventis Pasteur
 HGF derivatives -- Dompe
 hAPP vaccine -- Crucell
 Hib-hepatitis B vaccine -- Aventis Pasteur
 HIC 1
 HIP -- Altachem
 Hirudins -- Biopharma, Cangene, Dongkook, Japan Energy Corporation, Pharmacia Corporation, SIR International, Sanofi-Synthelabo, Sotragene, Rhein Biotech
 HIV edible vaccine -- ProdiGene
 HIV gp120 vaccine -- Chiron, Ajinomoto, GlaxoSmithKline, ID Vaccine, Progenics, VaxGen
 HIV gp120 vaccine gene therapy --
 HIV gp160 DNA vaccine -- PowderJect, Aventis Pasteur, Oncogen, Hyland Immuno, Protein Sciences
 HIV gp41 vaccine -- Panacos
 HIV HGP-30W vaccine -- CEL-SCI
 HIV immune globulin -- Abbott, Chiron
 HIV peptides -- American Home Products
 HIV vaccine -- Applied bioTech., Axis Genetics, Biogen, Bristol-Myers Squibb, Genentech, Korea Green Cross, NIS, Oncogen, Protein Sciences Corporation, Terumo, Tonen Corporation, Wyeth-Ayerst, Wyeth-Lederle Vaccines-Malvern, Advanced BioScience Laboratories, Bavarian Nordic, Bavarian Nordic/Statens Serum Institute, GeneCure, Immune Response, Progenics, Theron Biologics, United Biomedical, Chiron

FIG. 28M

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HIV vaccine vCP1433 -- Aventis Pasteur
 HIV vaccine vCP1452 -- Aventis Pasteur
 HIV vaccine vCP205 -- Aventis Pasteur
 HL-9 -- American BioScience
 HM-9239 -- Cytran
 HML-103 -- Hemosol
 HML-104 -- Hemosol
 HML-105 -- Hemosol
 HML-109 -- Hemosol
 HML-110 -- Hemosol
 HML-121 -- Hemosol
 hNLP -- Pharis
 Hookworm vaccine
 host-vector vaccines -- Henogen
 HPM 1 -- Chugai
 HPV vaccine -- MediGene
 HSA -- Meristem
 HSF -- StressGen
 HSP carriers -- Weizmann, Yeda, Peptor
 HSPPC-70 -- Antigenics
 HSPPC-96, pathogen-derived -- Antigenics
 HSV 863 -- Novartis
 HTLV-I DNA vaccine
 HTLV-I vaccine
 HTLV-II vaccine -- Access
 HU 901 -- Tanox
 Hu23F2G -- ICOS
 HuHMF1
 HumaLYM -- Intracell
 Human krebs statika -- Yamanouchi
 human monoclonal antibodies --
 Abgenix/Biogen, Abgenix/ Corixa,
 Abgenix/immunex, Abgenix/Lexicon,
 Abgenix/ Pfizer, Athersys/Medarex,
 Biogen/MorphoSys, CAT/Searle,
 Centocor/Medarex, Corixa/Kirin Brewery,
 Corixa/Medarex, Eos BioTech./Medarex,
 Eos/Xenerex, Exelixis/Protein Design
 Labs, ImmunoGen/ Raven, Medarex/
 B.Twelve, MorphoSys/ImmunoGen, XTL
 Biopharmaceuticals/Dyax,
 Human monoclonal antibodies --
 Medarex/Northwest Biotherapeutics,
 Medarex/Seattle Genetics
 human netrin-1 -- Exelixis
 human papillomavirus antibodies -- Epicyte
 Human papillomavirus vaccine -- Biotech
 Australia, IDEC, StressGen
 Human papillomavirus vaccine MEDI 501 --
 MedImmune/GlaxoSmithKline
 Human papillomavirus vaccine MEDI
 503/MEDI 504 --
 MedImmune/GlaxoSmithKline
 Human papillomavirus vaccine TA-CIN --
 Cantab Pharmaceuticals
 Human papillomavirus vaccine TA-HPV --
 Cantab Pharmaceuticals
 Human papillomavirus vaccine TH-GW --
 Cantab/GlaxoSmithKline
 human polyclonal antibodies -- Biosite/Eos
 BioTech./ Medarex
 human type II anti factor VIII monoclonal
 antibodies -- ThromboGenics
 humanised anti glycoprotein Ib murine
 monoclonal antibodies -- ThromboGenics
 HumaRAD -- Intracell
 HuMax EGFR -- Genmab
 HuMax-CD4 -- Medarex
 HuMax-IL15 -- Genmab
 HYB 190 -- Hybridon
 HYB 676 -- Hybridon
 I-125 Mab A33 -- Celltech
 Ibritumomab tiuxetan -- IDEC
 IBT-9401 -- Ibx
 IBT-9402 -- Ibx
 IC 14 -- ICOS
 Idarubicin anti-Ly-2.1 --
 IDEC 114 -- IDEC
 IDEC 131 -- IDEC
 IDEC 152 -- IDEC
 IDM 1 -- IDM
 IDPS -- Hollis-Eden Pharmaceuticals

FIG. 28N

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iduronate-2-sulfatase -- Transkaryotic
 Therapies
 IGF/IBP-2-13 -- Pharis
 IGN-101 -- Igeneon
 IK HIR02 -- Iketon
 IL-11 -- Genetics Institute/AHP
 IL-13-PE38 -- NeoPharm
 IL-17 receptor -- Immunex
 IL-18BP -- Yeda
 IL-1Hy1 -- Hyseq
 IL-1 β -- Celltech
 IL-1 β adjuvant -- Celltech
 IL-2 -- Chiron
 IL-2 + IL-12 -- Hoffman La-Roche
 IL-6/sIL-6R fusion -- Hadasit
 IL-6R derivative -- Tosoh
 IL-7-Dap 389 fusion toxin -- Ligand
 IL-21 -- Novo Nordisk, ZymoGenetics
 IM-862 -- Cytran
 IMC-1C11 -- ImClone
 imiglucerase -- Genzyme
 Immune globulin intravenous (human) --
 Hoffman La Roche
 immune privilege factor -- Proneuron
 Immunocal -- Immunotec
 Immunogene therapy -- Briana Bio-Tech
 Immunoliposomal 5-fluorodeoxyuridine-
 dipalmitate --
 immunosuppressant vaccine -- Aixlie
 immunotoxin -- Antisoma, NIH
 ImmuRAIT-Re-188 -- Immunomedics
 imreg-1 -- Imreg
 infertility -- Johnson & Johnson, E-TRANS
 Infliximab -- Centocor
 Influenza virus vaccine -- Aventis Pasteur,
 Protein Sciences
 inhibin -- Biotech Australia, Human
 Therapeutics
 Inhibitory G protein gene therapy
 INKP-2001 -- InKine
 Inolimomab -- Diaclone
 insulin -- AutoImmune, Altea, Biobras,
 BioSante, Bio-Tech. General, Chong Kun
 Dang, Emisphere, Flamel, Provalis, Rhein
 Biotech, TranXenoGen
 insulin (bovine) -- Novartis
 insulin analogue -- Eli Lilly
 Insulin Aspart -- Novo Nordisk
 insulin detemir -- Novo Nordisk
 insulin glargine -- Aventis
 insulin inhaled -- Inhale Therapeutics
 Systems, Alkermes
 insulin oral -- Inovax
 insulin, AeroDose -- AeroGen
 insulin, AERx -- Aradigm
 insulin, BEODAS -- Elan
 insulin, Biphasix -- Helix
 insulin, buccal -- Generex
 insulin, I2R -- Flemington
 insulin, intranasal -- Bentley
 insulin, oral -- Nobex, Unigene
 insulin, Orasome -- Endorex
 insulin, ProMaxx -- Epic
 insulin, Quadrant -- Elan
 insulin, recombinant -- Aventis
 insulin, Spiros -- Elan
 insulin, Transfersome -- IDEA
 insulin, Zymo, recombinant -- Novo Nordisk
 Insulintropin -- Scios
 Insulysin gene therapy --
 integrin antagonists -- Merck
 interferon (Alpha2) -- SRC VB VECTOR,
 Viragen, Dong-A, Hoffman La-Roche,
 Genentech
 interferon -- BioMedicines, Human Genome
 Sciences
 interferon (Alfa-n3) -- Interferon Sciences
 Intl.
 interferon (Alpha), Biphasix -- Helix

FIG. 280

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interferon (Alpha)—Amgen, BioNative,
 Novartis, Genzyme Transgenics,
 Hayashibara, Inhale Therapeutics
 Systems, Medusa, Flamel, Dong-A,
 GeneTrol, Nasteck, Shantha,
 Wassermann, LG Chem, Sumitomo,
 Aventis, Behring EGIS, Pepgen, Servier,
 Rhein Biotech,
 interferon (Alpha2A)
 interferon (Alpha2B) — Enzon, Schering-
 Plough, Biogen, IDEA
 interferon (Alpha-N1) — GlaxoSmithKline
 interferon (beta) — Rentschler, GeneTrol,
 Meristem, Rhein Biotech, Toray, Yeda,
 Daiichi, Mochida
 interferon (Beta1A) — Sero, Biogen
 interferon (beta1A), inhale — Biogen
 interferon (β1b)— Chiron
 interferon (tau)— Pepgen
 Interferon alfacon-1 — Amgen
 Interferon alpha-2a vaccine
 Interferon Beta 1b — Schering/Chiron,
 InterMune
 Interferon Gamma — Boehringer Ingelheim,
 Sheffield, Rentschler, Hayashibara
 interferon receptor, Type I — Sero
 interferon (Gamma1B) — Genentech
 Interferon-alpha-2b + ribavirin — Biogen,
 ICN
 Interferon-alpha-2b gene therapy —
 Schering-Plough
 Interferon-con1 gene therapy —
 interleukin-1 antagonists — Dompe
 Interleukin-1 receptor antagonist — Abbott
 Bioresearch, Pharmacia
 Interleukin-1 receptor type I — Immunex
 interleukin-1 receptor Type II — Immunex
 Interleukin-1 trap — Regeneron
 Interleukin-1-alpha — Immunex/Roche
 interleukin-2 — SRC VB VECTOR,
 Ajinomoto, Biomira, Chiron
 IL-2/ diphtheria toxin — Ligand
 Interleukin-3 — Cangene
 Interleukin-4 — Immunology Ventures,
 Sanofi Winthrop, Schering-Plough,
 Immunex/ Sanofi Winthrop, Bayer, Ono
 interleukin-4 + TNF-Alpha — NIH
 interleukin-4 agonist — Bayer
 interleukin-4 fusion toxin — Ligand
 Interleukin-4 receptor — Immunex, Immun
 Interleukin-6 — Ajinomoto, Cangene, Yeda,
 Genetics Institute, Novartis
 interleukin-6 fusion protein
 interleukin-6 fusion toxin — Ligand, Sero
 interleukin-7 — IC Innovations
 interleukin-7 receptor — Immunex
 interleukin-8 antagonists — Kyowa
 Hakko/Millennium/Pfizer
 interleukin-9 antagonists — Genaera
 Interleukin-10 — DNAX, Schering-Plough
 Interleukin-10 gene therapy —
 interleukin-12 — Genetics Institute, Hoffman
 La-Roche
 interleukin-13 — Sanofi
 interleukin-13 antagonists — AMRAD
 Interleukin-13-PE38QQR
 interleukin-15 — Immunex
 interleukin-16 — Research Corp
 Interleukin-18 — GlaxoSmithKline
 Interleukin-18 binding protein — Sero
 Ior-P3 — Center of Molecular Immunology
 IP-10 — NIH
 IPF — Metabolex
 IR-501 — Immune Response
 ISIS 9125 — Isis Pharmaceuticals
 ISURF No. 1554 — Millennium
 ISURF No. 1866 — Iowa State Univer.
 ITF-1697 — Italfarmaco
 IxC 162 — Ixion
 J 695 — Cambridge Antibody Tech.,
 Genetics Inst., Knoll
 Jagged + FGF — Repair

FIG. 28P

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JKC-362 -- Phoenix Pharmaceuticals
 JTP-2942 -- Japan Tobacco
 Juman monoclonal antibodies --
 Medarex/Raven
 K02 -- Axyx Pharmaceuticals
 Keliximab -- IDEC
 Keyhole limpet haemocyanin
 KGF -- Amgen
 KM 871 -- Kyowa
 KPI 135 -- Scios
 KPI-022 -- Scios
 Kringle 5
 KSB 304
 KSB-201 -- KS Biomedex
 L 696418 -- Merck
 L 703801 -- Merck
 L1 -- Acorda
 L-761191 -- Merck
 lactoferrin -- Meristem, Pharming, Agennix
 lactoferrin cardio -- Pharming
 LAG-3 -- Seroxo
 LAIT -- GEMMA
 LAK cell cytotoxin -- Arizona
 lamellarins -- PharmaMar/University of
 Malaga
 laminin A peptides -- NIH
 lanoteplase -- Genetics Institute
 laronidase -- BioMarin
 Lassa fever vaccine
 LCAT -- NIH
 LDP 01 -- Millennium
 LDP 02 -- Millennium
 Lecithinized superoxide dismutase --
 Seikagaku
 LeIF adjuvant -- Corixa
 leishmaniasis vaccine -- Corixa
 lenercept -- Hoffman La-Roche
 Lenograstim -- Aventis, Chugai
 lepirudin -- Aventis
 leptin -- Amgen, IC Innovations
 Leptin gene therapy -- Chiron Corporation
 leptin, 2nd-generation -- Amgen
 leridistim -- Pharmacia
 leuprolide, ProMaxx -- Epic
 leuprorelin, oral -- Unigene
 LeuTech -- Papatin
 LEX 032 -- SuperGen
 LiDEPT -- Novartis
 Lintuzumab (anti-CD33 MAb) -- Protein
 Design Labs
 lipase -- Altus Biologics
 lipid A vaccine -- EntreMed
 lipid-linked anchor Tech. -- ICRT, ID
 Biomedical
 liposome-CD4 Tech. -- Sheffield
 Listeria monocytogenes vaccine
 LMB 1
 LMB 7
 LMB 9 -- Battelle Memorial Institute, NIH
 LM-CD45 -- Cantab Pharmaceuticals
 lovastatin -- Merck
 LSA-3
 LT- β receptor -- Biogen
 lung cancer vaccine -- Corixa
 lusupultide -- Scios
 L-Vax -- AVAX
 LY 355455 -- Eli Lilly
 LY 366405 -- Eli Lilly
 LY-355101 -- Eli Lilly
 Lyme disease DNA vaccine -- Vical/Aventis
 Pasteur
 Lyme disease vaccine -- Aquila
 Biopharmaceuticals, Aventis, Pasteur,
 Symbicom, GlaxoSmithKline, Hyland
 Immuno, MedImmune
 Lymphocytic choriomeningitis virus vaccine
 lymphoma vaccine -- Biomira, Genitope
 LYP18
 lys plasminogen, recombinant
 Lysosomal storage disease gene therapy --
 Avigen
 lysostaphin -- Nutrition 21

FIG. 28Q

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M 23 -- Gruenenthal
 M1 monoclonal antibodies -- Acorda
 Therapeutics
 MA 16N7C2 -- Corvas Intl.
 malaria vaccine -- GlaxoSmithKline,
 AdProTech, Antigenics, Apovia, Aventis
 Pasteur, Axis Genetics, Behringwerke,
 CDCP, Chiron Vaccines, Genzyme
 Transgenics, Hawaii, MedImmune, NIH,
 NYU, Oxxon, Roche/Saramane, Biotech
 Australia, Rx Tech
 Malaria vaccine CDC/NIIMALVAC-1
 malaria vaccine, multicomponent
 mammaglobin -- Corixa
 mammastatin -- Biotherapeutics
 mannan-binding lectin -- NatlImmu
 mannan-MUC1 -- Psiron
 MAP 30
 Marinovir -- Phytera
 MARstem -- Maret
 MB-015 -- Mochida
 MBP -- ImmuLogic
 MCI-028 -- Mitsubishi-Tokyo
 MCIF -- Human Genome Sciences
 MDC -- Advanced BioScience -- Akzo
 Nobel, ICOS
 MDX 11 -- Medarex
 MDX 210 -- Medarex
 MDX 22 -- Medarex
 MDX 22
 MDX 240 -- Medarex
 MDX 33
 MDX 44 -- Medarex
 MDX 447 -- Medarex
 MDX H210 -- Medarex
 MDX RA -- Houston BioTech., Medarex
 ME-104 -- Pharmexa
 Measles vaccine
 Mecasermin -- Cephalon/Chiron, Chiron
 MEDI 488 -- MedImmune
 MEDI 500
 MEDI 507 -- BioTransplant
 melanin concentrating hormone --
 Neurocrine Biosciences
 melanocortins -- OMRF
 Melanoma monoclonal antibodies -- Viragen
 melanoma vaccine -- GlaxoSmithKline,
 Akzo Nobel, Avant, Aventis Pasteur,
 Bavarian Nordic, Biovector, CancerVax,
 Genzyme Molecular Oncology, Humbolt,
 ImClone Systems, Memorial, NYU, Oxxon
 Melanoma vaccine Magevac -- Therion
 memory enhancers -- Scios
 meningococcal B vaccine -- Chiron
 meningococcal vaccine -- CAMR
 Meningococcal vaccine group B conjugate -
 - North American Vaccine
 Meningococcal vaccine group B
 recombinant -- BioChem Vaccines,
 Microscience
 Meningococcal vaccine group Y conjugate -
 - North American Vaccine
 Meningococcal vaccine groups A B and C
 conjugate -- North American Vaccine
 Mepolizumab -- GlaxoSmithKline
 Metastatin -- EntreMed, Takeda
 Met-CkB7 -- Human Genome Sciences
 met-enkephalin -- TNI
 METH-1 -- Human Genome Sciences
 methioninase -- AntiCancer
 Methionine lyase gene therapy --
 AntiCancer
 Met-RANTES -- Genexa Biomedical,
 Seroxo
 Metreleptin
 Microtubule inhibitor MAb
 Immunogen/Abgenix
 MGDF -- Kirin
 MGTV -- Progenics
 micrin -- Endocrine
 microplasmin -- ThromboGenics
 MIF -- Genetics Institute

FIG. 28R

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migration inhibitory factor -- NIH	MAb 45-2D9- -- haematoporphyrin conjugate
Mim CD4.1 -- Xycte Therapies	MAb 4B4
mirostipen -- Human Genome Sciences	MAb 4E3-CPA conjugate -- BCM Oncologia
Mitumomab (BEC-2) -- ImClone Systems, Merck KGaA	MAb 4E3-daunorubicin conjugate
MK 852 -- Merck	MAb 50-6
MLN 1202 (Anti-CCR2 monoclonal antibody) -- Millenium Pharmaceuticals	MAb 50-61A -- Institut Pasteur
Mobenakin -- NIS	MAb 5A8 -- Biogen
molgramostim -- Genetics Institute, Novartis	MAb 791T/36-methotrexate conjugate
monoclonal antibodies -- Abgenix/Celltech, Immusol/ Medarex, Viragen/ Roslin Institute, Cambridge Antibody Tech./Elan	MAb 7c11.e8
MAb 108 --	MAb 7E11 C5-selenocystamine conjugate
MAb 10D5 --	MAb 93KA9 -- Novartis
MAb 14.18-interleukin-2 immunocytokine -- Lexigen	MAb A5B7-cisplatin conjugate -- Biodynamics Research, Pharmacia
MAb 14G2a --	MAb A5B7-I-131
MAb 15A10 --	MAb A7
MAb 170 -- Biomira	MAb A717 -- Exocell
MAb 177Lu CC49 --	MAb A7-zinostatin conjugate
MAb 17F9	MAb ABX-RB2 -- Abgenix
MAb 1D7	MAb ACA 11
MAb 1F7 -- Immune Network	MAb AFP-I-131 -- Immunomedics
MAb 1H10-doxorubicin conjugate	MAb AP1
MAb 26-2F	MAb AZ1
MAb 2A11	MAb B3-LysPE40 conjugate
MAb 2E1 -- RW Johnson	MAb B4 -- United Biomedical
MAb 2F5	MAb B43 Genistein-conjugate
MAb 31.1 -- International BioImmune Systems	MAb B43.13-Tc-99m -- Biomira
MAb 32 -- Cambridge Antibody Tech., Peptech	MAb B43-PAP conjugate
MAb 323A3 -- Centocor	MAb B4G7-gelonin conjugate
MAb 3C5	MAb BCM 43-daunorubicin conjugate -- BCM Oncologia
MAb 3F12	MAb BIS-1
MAb 3F8	MAb BMS 181170 -- Bristol-Myers Squibb
MAb 42/6	MAb BR55-2
MAb 425 -- Merck KGaA	MAb BW494
MAb 447-52D -- Merck Sharp & Dohme	MAb C 242-DM1 conjugate -- ImmunoGen
	MAb C242-PE conjugate
	MAb c30-6
	MAb CA208-cytorhodin-S conjugate -- Hoechst Japan
	MAb CC49 -- Enzo

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MAb ch14.18 --	MAb LL2-I-131 -- Immunomedics
MAb CH14.18-GM-CSF fusion protein --	MAb LL2-Y-90
Lexigen	MAb LS2D617 -- Hybritech
MAb chCE7	MAb LYM-1-gelonin conjugate
MAb CI-137 -- AMRAD	MAb LYM-1-I-131
MAb cisplatin conjugate	MAb LYM-1-Y-90
MAb CLB-CD19	MAb LYM-2 -- Peregrine
MAb CLB-CD19v	MAb M195
MAb CLL-1 -- Peregrine	MAb M195-bismuth 213 conjugate --
MAb CLL-1-GM-CSF conjugate	Protein Design Labs
MAb CLL-1-IL-2 conjugate -- Peregrine	MAb M195-gelonin conjugate
MAb CLN IgG -- doxorubicin conjugates	MAB M195-I-131
MAB conjugates -- Tanox	MAB M195-Y-90
MAB D612	MAB MA 33H1 -- Sanofi
MAB Dal B02	MAB MAD11
MAB DC101 -- ImClone	MAB MGB2
MAB EA 1 --	MAB MINT5
MAB EC708 -- Biovation	MAB MK2-23
MAB EP-5C7 -- Protein Design Labs	MAB MOC31 ETA(252-613) conjugate
MAB ERIC-1 -- ICRT	MAB MOC-31-In-111
MAB F105 gene therapy	MAB MOC-31-PE conjugate
MAB FC 2.15	MAB MR6 --
MAB G250 -- Centocor	MAB MRK-16 -- Aventis Pasteur
MAB GA6	MAB MS11G6
MAB GA733	MAB MX-DTPA BrE-3
MAB Gliomab-H -- Viventia Biotech	MAB MY9
MAB HB2-saporin conjugate	MAB Nd2 -- Tosoh
MAB HD 37 --	MAB NG-1 -- Hygeia
MAB HD37-ricin chain-A conjugate	MAB NM01 -- Nissin Food
MAB HNK20 -- Acambis	MAB OC 125
MAB huN901-DM1 conjugate --	MAB OC 125-CMA conjugate
ImmunoGen	MAB OKI-1 -- Ortho-McNeil
MAB I-131 CC49 -- Corixa	MAB OX52 -- Bioproducts for Science
MAB ICO25	MAB PMA5
MAB ICR12-CPG2 conjugate	MAB PR1
MAB ICR-62	MAB prost 30
MAB IRac-ricin A conjugate	MAB R-24
MAB K1	MAB R-24 α Human GD3 -- Celltech
MAB KS1-4-methotrexate conjugate	MAB RFB4-ricin chain A conjugate
MAB L6 -- Bristol-Myers Squibb, Oncogen	MAB RFT5-ricin chain A conjugate
MAB LICO 16-88	MAB SC 1

FIG. 28T

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MAb SM-3 -- ICRT
 MAb SMART 1D10 -- Protein Design Labs
 MAb SMART ABL 364 -- Novartis
 MAb SN6f
 MAb SN6f-deglycosylated ricin A chain conjugate --
 MAb SN6j
 MAb SN7-ricin chain A conjugate
 MAb T101-Y-90 conjugate -- Hybritech
 MAb T-88 -- Chiron
 MAb TB94 -- Cancer Immunobiology
 MAb TEC 11
 MAb TES-23 -- Chugai
 MAb TM31 -- Avant
 MAb TNT-1 -- Cambridge Antibody Tech., Peregrine
 MAb TNT-3
 MAb TNT-3 -- IL2 fusion protein --
 MAb TP3-At-211
 MAb TP3-PAP conjugate --
 MAb UJ13A -- ICRT
 MAb UN3
 MAb ZME-018-gelonin conjugate
 MAb-BC2 -- GlaxoSmithKline
 MAb-DM1 conjugate -- ImmunoGen
 MAb-ricin-chain-A conjugate -- XOMA
 MAb-temoporfin conjugates
 Monopharm C -- Viventia Biotech
 montepelase -- Eisai
 montirelin hydrate -- Gruenenthal
 morotocog alfa -- Genetics Institute
 Morotocog-alfa -- Pharmacia
 MP 4
 MP-121 -- Biopharm
 MP-52 -- Biopharm
 MRA -- Chugai
 MS 28168 -- Mitsui Chemicals, Nihon Schering
 MSH fusion toxin -- Ligand
 MSI-99 -- Genæra
 MT 201 -- Micromet
 Muc-1 vaccine -- Corixa
 mucosal tolerance -- Aberdeen
 mullerian inhibiting subst
 muplestim -- Genetics Institute, Novartis,
 DSM Anti-Infectives
 murine MAb -- KS Biomedix
 Mutant somatropin -- JCR Pharmaceutical
 MV 833 -- Toagosei
 Mycoplasma pulmonis vaccine
 Mycoprex -- XOMA
 myeloperoxidase -- Henogen
 myostatin -- Genetics Institute
 Nacolomab tafanatox -- Pharmacia
 Nagrecor -- Scios
 nagrestipen -- British Biotech
 NAP-5 -- Corvas Intl.
 NAPc2 -- Corvas Intl.
 nartograstim -- Kyowa
 Natalizumab -- Protein Design Labs
 Nateplase -- NIH, Nihon Schering
 nateplase -- Schering AG
 NBI-3001 -- Neurocrine Biosci.
 NBI-5788 -- Neurocrine Biosci.
 NBI-6024 -- Neurocrine Biosci.
 Nef inhibitors -- BRI
 Neisseria gonorrhoea vaccine -- Antex Biologics
 Neomycin B-arginine conjugate
 Nerelimomab -- Chiron
 Nerve growth factor -- Amgen -- Chiron, Genentech
 Nerve growth factor gene therapy
 nesiritide citrate -- Scios
 neuregulin-2 -- CeNeS
 neurocan -- NYU
 neuronal delivery system -- CAMR
 Neurophil inhibitory Factor -- Corvas
 Neuroprotective vaccine -- University of Auckland
 neurotrophic chimaeras -- Regeneron
 neurotrophic factor -- NsGene, CereMedix

FIG. 28U

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NeuroVax -- Immune Response
 neurturnin -- Genentech
 neutral endopeptidase -- Genentech
 NGF enhancers -- NeuroSearch
 NHL vaccine -- Large Scale Biology
 NIP45 -- Boston Life Sciences
 NKI-B20
 NM 01 -- Nissin Food
 NMI-139 -- NitroMed
 NMMP -- Genetics Institute
 NN-2211 -- Novo Nordisk
 Noggin -- Regeneron
 Nonacog alfa
 Norelin -- Biostar
 Norwalk virus vaccine
 NRLU 10 -- NeoRx
 NRLU 10 PE -- NeoRx
 NT-3 -- Regeneron
 NT-4/5 -- Genentech
 NU 3056
 NU 3076
 NX 1838 -- Gilead Sciences
 NY ESO-1/CAG-3 antigen -- NIH
 NYVAC-7 -- Aventis Pasteur
 NZ-1002 -- Novazyme
 obesity therapy -- Nobex
 OC 10426 -- Ontogen
 OC 144093 -- Ontogen
 OCIF -- Sankyo
 Oct-43 -- Otsuka
 Odulimomab -- Immunotech
 OK PSA - liposomal
 OKT3-gamma-1-ala-ala
 OM 991
 OM 992
 Omalizumab -- Genentech
 oncoimmunin-L -- NIH
 Oncolysin B -- ImmunoGen
 Oncolysin CD6 -- ImmunoGen
 Oncolysin M -- ImmunoGen
 Oncolysin S -- ImmunoGen
 Oncophage -- Antigenics
 Oncostatin M -- Bristol-Myers Squibb
 OncoVax-CL -- Jenner Biotherapies
 OncoVax-P -- Jenner Biotherapies
 onercept -- Yeda
 onychomycosis vaccine -- Boehringer
 Ingelheim
 opebecan -- XOMA
 opioids -- Arizona
 Oprelvekin -- Genetics Institute
 Oregovomab -- AltaRex
 Org-33408 b-- Akzo Nobel
 Orlip DP -- EpiCept
 oryzacystatin
 OSA peptides -- GenSci Regeneration
 osteoblast-cadherin GF -- Pharis
 Osteocalcin-thymidine kinase gene therapy
 osteogenic protein -- Curis
 osteopontin -- OraPharma
 osteoporosis peptides -- Integra, Telios
 osteoprotegerin -- Amgen, SnowBrand
 otitis media vaccines -- Antex Biologics
 ovarian cancer -- University of Alabama
 OX40-IgG fusion protein -- Cantab, Xenova
 P 246 -- Diatide
 P 30 -- Alfacell
 p1025 -- Active Biotech
 P-113^A -- Demegen
 P-16 peptide -- Transition Therapeutics
 p43 -- Ramot
 P-50 peptide -- Transition Therapeutics
 p53 + RAS vaccine -- NIH, NCI
 PACAP(1-27) analogue
 paediatric vaccines -- Chiron
 Pafase -- ICOS
 PAGE-4 plasmid DNA -- IDEC
 PAI-2 -- Biotech Australia, Human
 Therapeutics
 Palifermin (keratinocyte growth factor) --
 Amgen
 Palivizumab -- MedImmune

FIG. 28V

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PAM 4 -- Merck
 pamiteplase -- Yamanouchi
 pancreatin, Minitabs -- Eurand
 Pangen -- Fournier
 Pantarin -- Selective Genetics
 Parainfluenza virus vaccine -- Pharmacia,
 Pierre Fabre
 paraoxanase -- Esperion
 parathyroid hormone -- Abiogen, Korea
 Green Cross
 Parathyroid hormone (1-34) --
 Chugai/Suntory
 Parkinson's disease gene therapy -- Cell
 Genesys/ Ceregene
 Parvovirus vaccine -- MedImmune
 PCP-Scan -- Immunomedics
 PDGF -- Chiron
 PDGF cocktail -- Theratechnologies
 peanut allergy therapy -- Dynavax
 PEG anti-ICAM MAb -- Boehringer
 Ingelheim
 PEG asparaginase -- Enzon
 PEG glucocerebrosidase
 PEG hirudin -- Knoll
 PEG interferon-alpha-2a -- Roche
 PEG interferon-alpha-2b + ribavirin --
 Biogen, Enzon, ICN Pharmaceuticals,
 Schering-Plough
 PEG MAb A5B7 --
 Pegacaristim -- Amgen -- Kirin Brewery --
 ZymoGenetics
 Pegaldesleukin -- Research Corp
 pegaspargase -- Enzon
 pegfilgrastim -- Amgen
 PEG-interferon Alpha -- Viragen
 PEG-interferon Alpha 2A -- Hoffman La-
 Roche
 PEG-interferon Alpha 2B -- Schering-
 Plough
 PEG-r-hirudin -- Abbott
 PEG-rHuMGDF -- Amgen
 PEG-uricase -- Mountain View
 Pegvisomant -- Genentech
 PEGylated proteins, PolyMASC -- Valentis
 PEGylated recombinant native human leptin
 -- Roche
 Pentumomab
 Penetratin -- Cyclacel
 Pepscan -- Antisoma
 peptide G -- Peptech, ICRT
 peptide vaccine -- NIH ,NCI
 Pexelizumab
 pexiganan acetate -- Genaera
 Pharmaprojects No. 3179 -- NYU
 Pharmaprojects No. 3390 -- Ernest Orlando
 Pharmaprojects No. 3417 -- Sumitomo
 Pharmaprojects No. 3777 -- Acambis
 Pharmaprojects No. 4209 -- XOMA
 Pharmaprojects No. 4349 -- Baxter Intl.
 Pharmaprojects No. 4651
 Pharmaprojects No. 4915 -- Avanir
 Pharmaprojects No. 5156 -- Rhizogenics
 Pharmaprojects No. 5200 -- Pfizer
 Pharmaprojects No. 5215 -- Origene
 Pharmaprojects No. 5216 -- Origene
 Pharmaprojects No. 5218 -- Origene
 Pharmaprojects No. 5267 -- ML
 Laboratories
 Pharmaprojects No. 5373 -- MorphoSys
 Pharmaprojects No. 5493 -- Metabolex
 Pharmaprojects No. 5707 -- Genentech
 Pharmaprojects No. 5728 -- Autogen
 Pharmaprojects No. 5733 -- BioMarin
 Pharmaprojects No. 5757 -- NIH
 Pharmaprojects No. 5765 -- Gryphon
 Pharmaprojects No. 5830 -- AntiCancer
 Pharmaprojects No. 5839 -- Dyax
 Pharmaprojects No. 5849 -- Johnson &
 Johnson
 Pharmaprojects No. 5860 -- Mitsubishi-
 Tokyo

FIG. 28W

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Pharmaprojects No. 5869 -- Oxford GlycoSciences
 Pharmaprojects No. 5883 -- Asahi Brewery
 Pharmaprojects No. 5947 -- StressGen
 Pharmaprojects No. 5961 -- Theratechnologies
 Pharmaprojects No. 5962 -- NIH
 Pharmaprojects No. 5966 -- NIH
 Pharmaprojects No. 5994 -- Pharming
 Pharmaprojects No. 5995 -- Pharming
 Pharmaprojects No. 6023 -- IMMUCON
 Pharmaprojects No. 6063 -- Cytoclonal
 Pharmaprojects No. 6073 -- SIDDCO
 Pharmaprojects No. 6115 -- Genzyme
 Pharmaprojects No. 6227 -- NIH
 Pharmaprojects No. 6230 -- NIH
 Pharmaprojects No. 6236 -- NIH
 Pharmaprojects No. 6243 -- NIH
 Pharmaprojects No. 6244 -- NIH
 Pharmaprojects No. 6281 -- Senetek
 Pharmaprojects No. 6365 -- NIH
 Pharmaprojects No. 6368 -- NIH
 Pharmaprojects No. 6373 -- NIH
 Pharmaprojects No. 6408 -- Pan Pacific
 Pharmaprojects No. 6410 -- Athersys
 Pharmaprojects No. 6421 -- Oxford GlycoSciences
 Pharmaprojects No. 6522 -- Maxygen
 Pharmaprojects No. 6523 -- Pharis
 Pharmaprojects No. 6538 -- Maxygen
 Pharmaprojects No. 6554 -- APALEXO
 Pharmaprojects No. 6560 -- Ardana
 Pharmaprojects No. 6562 -- Bayer
 Pharmaprojects No. 6569 -- Eos
 Phenoxazine
 Phenylase -- Ilex
 Pigment epithelium derived factor -- plasminogen activator inhibitor-1, recombinant -- DuPont Pharmaceuticals
 Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda
 plasminogen-related peptides -- Bio-Tech. General/MGH
 platelet factor 4 -- RepliGen
 Platelet-derived growth factor -- Amgen -- ZymoGenetics
 plusonemin -- Hayashibara
 PMD-2850 -- Protherics
 Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur
 Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector
 PR1A3
 PR-39
 pralmorelin -- Kaken
 Pretarget-Lymphoma -- NeoRx
 Priliximab -- Centocor
 PRO 140 -- Progenics
 PRO 2000 -- Procept
 PRO 367 -- Progenics
 PRO 542 -- Progenics
 pro-Apo A-I -- Esperion
 prolactin -- Genzyme
 Prosaptide TX14(A) -- Bio-Tech. General
 prostate cancer antibodies -- Immunex, UroCor
 prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics
 prostate cancer immunotherapeutics -- The PSMA Development Company
 prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner
 Biotherapies, Therion Biologics

FIG. 28X

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prostate-specific antigen -- Entremed
 protein A -- RepliGen
 protein adhesives -- Enzon
 protein C -- Baxter Intl., PPL Therapeutics,
 ZymoGenetics
 protein C activator -- Gilead Sciences
 protein kinase R antagonists -- NIH
 protirelin -- Takeda
 protocadherin 2 -- Caprion
 Pro-urokinase -- Abbott, Bristol-Myers
 Squibb, Dainippon, Tosoh -- Welfide
 P-selectin glycoprotein ligand-1 -- Genetics
 Institute
 pseudomonal infections -- InterMune
 Pseudomonas vaccine -- CytoVax
 PSGL-Ig -- American Home Products
 PSP-94 -- Procyon
 PTH 1-34 -- Nobex
 Quilimmune-M -- Antigenics
 R 744 -- Roche
 R 101933
 R 125224 -- Sankyo
 RA therapy -- Cardion
 Rabies vaccine recombinant -- Aventis
 Pasteur, BioChem Vaccines, Kaketsuken
 Pharmaceuticals
 RadioTheraCIM -- YM BioSciences
 Ramot project No. 1315 -- Ramot
 Ramot project No. K-734A -- Ramot
 Ramot project No. K-734B -- Ramot
 Ranibizumab (Anti-VEGF fragment) --
 Genentech
 RANK -- Immunex
 ranpirinase -- Alfacell
 ranpirinase-anti-CD22 MAb -- Alfacell
 RANTES inhibitor -- Milan
 RAPID drug delivery systems -- ARIAD
 rasburicase -- Sanofi
 rBPI-21, topical -- XOMA
 RC 529 -- Corixa
 rCFTR -- Genzyme Transgenics

RD 62198
 rDnase -- Genentech
 RDP-58 -- SangStat
 ReceptTox-Fce -- Keryx
 ReceptTox-GnRH -- Keryx, MTR
 Technologies
 ReceptTox-MBP -- Keryx, MTR
 Technologies
 recFSH -- Akzo Nobel, Organon
 REGA 3G12
 Regavirumab -- Teijin
 relaxin -- Connetics Corp
 Renal cancer vaccine -- MacroPharm
 repifermin -- Human Genome Sciences
 Respiratory syncytial virus PFP-2 vaccine --
 Wyeth-Lederle
 Respiratory syncytial virus vaccine --
 GlaxoSmithKline, Pharmacia, Pierre Fabre
 Respiratory syncytial virus vaccine
 inactivated
 Respiratory syncytial virus-parainfluenza
 virus vaccine -- Aventis Pasteur,
 Pharmacia
 Reteplase -- Boehringer Mannheim,
 Hoffman La-Roche
 Retropep -- Retroscreen
 RFB4 (dsFv) PE38
 RFI 641 -- American Home Products
 RFTS -- UAB Research Foundation
 RG 12986 -- Aventis Pasteur
 RG 83852 -- Aventis Pasteur
 RG-1059 -- RepliGen
 rGCR -- NIH
 rGLP-1 -- Restoragen
 rGRF -- Restoragen
 rh Insulin -- Eli Lilly
 RHAMM targeting peptides -- Cangene
 rHb1.1 -- Baxter Intl.
 rhCC10 -- Claragen
 rhCG -- SeroNo
 Rheumatoid arthritis gene therapy

FIG. 28Y

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Rheumatoid arthritis vaccine -- Veterans
 Affairs Medical Center
 rhLH -- Serono
 Ribozyme gene therapy -- Genset
 Rickettsial vaccine recombinant
 RIGScan CR -- Neoprobe
 RIP-3 -- Rigel
 Rituximab -- Genentech
 RK-0202 -- RxKinetix
 RLT peptide -- Esperion
 rM/NEI -- IVAX
 rmCRP -- Immtech
 RN-1001 -- Renovo
 RN-3 -- Renovo
 RNase conjugate -- Immunomedics
 RO 631908 -- Roche
 Rotavirus vaccine -- Merck
 RP 431 -- DuPont Pharmaceuticals
 RP-128 -- Resolution
 RPE65 gene therapy --
 RPR 110173 -- Aventis Pasteur
 RPR 115135 -- Aventis Pasteur
 RPR 116258A -- Aventis Pasteur
 rPSGL-Ig -- American Home Products
 r-SPC surfactant -- Byk Gulden
 RSV antibody -- Medimmune
 Ruplizumab -- Biogen
 rV-HER-2/neu -- Therion Biologics
 SA 1042 -- Sankyo
 sacrosidase -- Orphan Medical
 Sant 7
 Sargramostim -- Immunex
 saruplase -- Gruenenthal
 Satumomab -- Cytogen
 SB 1 -- COR Therapeutics
 SB 207448 -- GlaxoSmithKline
 SB 208651 -- GlaxoSmithKline
 SB 240683 -- GlaxoSmithKline
 SB 249415 -- GlaxoSmithKline
 SB 249417 -- GlaxoSmithKline
 SB 6 -- COR Therapeutics
 SB RA 31012 --
 SC 56929 -- Pharmacia
 SCA binding proteins -- Curis, Enzon
 scFv(14E1)-ETA Berlex Laboratories,
 Schering AG
 ScFv(FRP5)-ETA --
 ScFv6C6-PE40 --
 SCH 55700 -- Celltech
 Schistosomiasis vaccine -- Glaxo
 Wellcome/Medeva, Brazil
 SCPF -- Advanced Tissue Sciences
 scuPA-suPAR complex -- Hadasit
 SD-9427 -- Pharmacia
 SDF-1 -- Ono
 SDZ 215918 -- Novartis
 SDZ 280125 -- Novartis
 SDZ 89104 -- Novartis
 SDZ ABL 364 -- Novartis
 SDZ MMA 383 -- Novartis
 Secretin -- Ferring, Repligen
 serine protease inhbs -- Pharis
 sermorelin acetate -- Sero
 SERP-1 -- Viron
 sertenef -- Dainippon
 serum albumin, Recombinant human --
 Aventis Behring
 serum-derived factor -- Hadasit
 Sevirumab -- Novartis
 SGN 14 -- Seattle Genetics
 SGN 15 -- Seattle Genetics
 SGN 17/19 -- Seattle Genetics
 SGN 30 -- Seattle Genetics
 SGN-10 -- Seattle Genetics
 SGN-11 -- Seattle Genetics
 SH 306 -- DuPont Pharmaceuticals
 Shanvac-B -- Shantha
 Shigella flexneri vaccine -- Avant, Acambis,
 Novavax
 Shigella sonnei vaccine --
 siCAM-1 -- Boehringer Ingelheim
 Silteplase -- Genzyme

FIG. 28Z

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SIV vaccine -- Endocon, Institut Pasteur
 SK 896 -- Sanwa Kagaku Kenkyusho
 SK-827 -- Sanwa Kagaku Kenkyusho
 Skeletex -- CellFactors
 SKF 106160 -- GlaxoSmithKline
 S-nitroso-AR545C --
 SNTP -- Active Biotech
 somatomedin-1 -- GroPep, Mitsubishi-
 Tokyo, NIH
 somatomedin-1 carrier protein -- Insmed
 somatostatin -- Ferring
 Somatotropin/
 Human Growth Hormone -- Bio-Tech.
 General, Eli Lilly
 somatropin -- Bio-Tech. General, Alkermes,
 ProLease, Aventis Behring, Biovector,
 Cangene, Dong-A, Eli Lilly, Emisphere,
 Enact, Genentech, Genzyme Transgenics,
 Grandis/InfiMed, CSL, InfiMed, MacroMed,
 Novartis, Novo Nordisk, Pharmacia
 Serono, TranXenoGen
 somatropin derivative -- Schering AG
 somatropin, AIR -- Eli Lilly
 Somatropin, inhaled -- Eli Lilly/Alkermes
 somatropin, Kabi -- Pharmacia
 somatropin, Orasome -- Novo Nordisk
 Sonermin -- Daiippon Pharmaceutical
 SP(V5.2)C -- Supertek
 SPf66
 sphingomyelinase -- Genzyme
 SR 29001 -- Sanofi
 SR 41476 -- Sanofi
 SR-29001 -- Sanofi
 SS1(dsFV)-PE38 -- NeoPharm
 β 2 microglobulin -- Avidex
 β 2-microglobulin fusion proteins -- NIH
 β -amyloid peptides -- CeNeS
 β -defensin -- Pharis
 Staphylococcus aureus infections --
 InhibiTex/ZLB
 Staphylococcus aureus vaccine conjugate --
 Nabi
 Staphylococcus therapy -- Tripep
 Staphylokinase -- Biovation, Prothera,
 Thrombogenetics
 Streptococcal A vaccine -- M6
 Pharmaceuticals, North American Vaccine
 Streptococcal B vaccine -- Microscience
 Streptococcal B vaccine recombinant --
 Biochem Vaccines
 Streptococcus pyogenes vaccine
 STRL-33 -- NIH
 Subalin -- SRC VB VECTOR
 SUIIS -- United Biomedical
 SUIIS-LHRH -- United Biomedical
 SUN-E3001 -- Suntory
 super high affinity monoclonal antibodies --
 YM BioSciences
 Superoxide dismutase -- Chiron, Enzon,
 Ube Industries, Bio-Tech, Yeda
 superoxide dismutase-2 -- OXIS
 suppressin -- UAB Research Foundation
 SY-161-P5 -- ThromboGenics
 SY-162 -- ThromboGenics
 Systemic lupus erythematosus vaccine --
 MedClone/VivoRx
 T cell receptor peptides -- Xoma
 T cell receptor peptide vaccine
 T4N5 liposomes -- AGI Dermatics
 TACI, soluble -- ZymoGenetics
 targeted apoptosis -- Antisoma
 tasonermin -- Boehringer Ingelheim
 TASP
 TASP-V
 Tat peptide analogues -- NIH
 TBP I -- Yeda
 TBP II
 TBV25H -- NIH
 Tc 99m ior cea1 -- Center of Molecular
 Immunology
 Tc 99m P 748 -- Diatide

FIG. 28AA

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Tc 99m votumab -- Intracell
 Tc-99m rh-Annexin V -- Theseus Imaging
 teceleukin -- Biogen
 tenecteplase -- Genentech
 Teriparatide -- Armour Pharmaceuticals,
 Asahi Kasei, Eli Lilly
 terlipressin -- Ferring
 testisin -- AMRAD
 Tetra fibrin -- Roche
 TFPI -- EntrelMed
 tgD-IL-2 -- Takeda
 TGF-Alpha -- ZymoGenetics
 TGF- β -- Kolon
 TGF- β 2 -- Insmad
 TGF- β 3 -- OSI
 Thalassemia gene therapy -- Crucell
 TheraCIM-h-R3 -- Center of Molecular
 Immunology, YM BioSciences
 Theradigm-HBV -- Epimmune
 Theradigm-HPV -- Epimmune
 Theradigm-malaria -- Epimmune
 Theradigm-melanoma -- Epimmune
 TheraFab -- Antisoma
 ThGRF 1-29 -- Theratechnologies
 ThGRF 1-44 -- Theratechnologies
 Thrombin receptor activating peptide --
 Abbott
 thrombomodulin -- Iowa, Novocastra
 Thrombopoietin -- Dragon Pharmaceuticals,
 Genentech
 thrombopoietin, Pliva -- Recepton
 Thrombospondin 2 --
 thrombostatin -- Thromgen
 thymalfasin -- SciClone
 thymocartin -- Gedeon Richter
 thymosin Alpha1 -- NIH
 thyroid stimulating hormone -- Genzyme
 tICAM-1 -- Bayer
 Tick anticoagulant peptide -- Merck
 TIF -- Xoma
 Tifacogin -- Chiron, NIS, Pharmacia
 Tissue factor -- Genentech
 Tissue factor pathway inhibitor
 TJN-135 -- Tsumura
 TM 27 -- Avant
 TM 29 -- Avant
 TMC-151 -- Tanabe Seiyaku
 TNF tumour necrosis factor -- Asahi Kasei
 TNF Alpha -- CytImmune
 TNF antibody -- Johnson & Johnson
 TNF binding protein -- Amgen
 TNF degradation product -- Oncotech
 TNF receptor -- Immunex
 TNF receptor 1, soluble -- Amgen
 TNF Tumour necrosis factor-alpha -- Asahi
 Kasei, Genentech, Mochida
 TNF-Alpha inhibitor -- Tripep
 TNFR:Fc gene therapy -- Targeted Genetics
 TNF-SAM2
 Tolerimab -- Innogenetics
 Toxoplasma gondii vaccine --
 GlaxoSmithKline
 TP 9201 -- Telios
 TP10 -- Avant
 TP20 -- Avant
 tPA -- Centocor
 trafermin -- Scios
 TRAIL/Apo2L -- Immunex
 TRAIL-R1 MAb -- Cambridge Antibody
 Technologies
 transferrin-binding proteins -- CAMR
 Transforming growth factor-beta-1 --
 Genentech
 transport protein -- Genesis
 Trastuzumab -- Genentech
 TRH -- Ferring
 Triabin -- Schering AG
 Triconal
 Triflavin
 troponin I -- Boston Life Sciences
 TRP-2^A -- NIH
 trypsin inhibitor -- Mochida

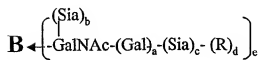
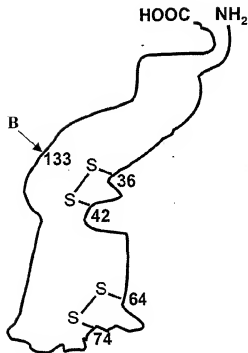
FIG. 28BB

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TSP-1 gene therapy --	Vascular endothelial growth factors -- R&D
TT-232	Systems
TTS-CD2 -- Active Biotech	vascular targeting agents -- Peregrine
Tuberculosis vaccine -- Aventis Pasteur,	vasopermeation enhancement agents --
Genesis	Peregrine
Tumor Targeted Superantigens -- Active	vasostatin -- NIH
Biotech -- Pharmacia	VCL -- Bio-Tech. General
tumour vaccines -- PhotoCure	VEGF -- Genentech, Scios
tumour-activated prodrug antibody	VEGF inhibitor -- Chugai
conjugates -- Millennium/ImmunoGen	VEGF-2 -- Human Genome Sciences
tumstatin -- ILEX	VEGF-Trap -- Regeneron
Tuvirumab -- Novartis	viscumin, recombinant -- Madaus
TV-4710 -- Teva	Vitaxin
TWEAK receptor -- Immunex	Vitrax -- ISTA Pharmaceuticals
TXU-PAP	West Nile virus vaccine -- Bavarian Nordic
TY-10721 -- TOA Eiyo	WP 652
Type I diabetes vaccine -- Research Corp	WT1 vaccine -- Corixa
Typhoid vaccine CVD 908	WX-293 -- Wilex BioTech.
U 143677 -- Pharmacia	WX-360 -- Wilex BioTech.
U 81749 -- Pharmacia	WX-UK1 -- Wilex BioTech.
UA 1248 -- Arizona	XMP-500 -- XOMA
UGIF -- Sheffield	XomaZyme-791 -- XOMA
UIC 2	XTL 001 -- XTL Biopharmaceuticals
UK 101	XTL 002 -- XTL Biopharmaceuticals
UK-279276 -- Corvas Intl.	yeast delivery system -- GlobelImmune
urodilatin -- Pharis	Yersinia pestis vaccine
urofollitrophin -- Serono	YIGSR-Stealth -- Johnson & Johnson
Urokinase -- Abbott	Yissum Project No. D-0460 -- Yissum
uteroferin -- Pepgen	YM 207 -- Yamanouchi
V 20 -- GLYCODesign	YM 337 -- Protein Design Labs
V2 vasopressin receptor gene therapy	Yttrium-90 labelled biotin
vaccines -- Active Biotech	Yttrium-90-labeled anti-CEA MAb T84.66 --
Varicella zoster glycoprotein vaccine --	ZD 0490 -- AstraZeneca
Research Corporation Technologies	ziconotide -- Elan
Varicella zoster virus vaccine live -- Cantab	ZK 157138 -- Berlex Laboratories
Pharmaceuticals	Zolimomab arixox
Vascular endothelial growth factor --	Zorcell -- Immune Response
Genentech, University of California	ZRXL peptides -- Novartis

FIG. 28CC

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, sialyl or oligosialyl

FIG. 29A

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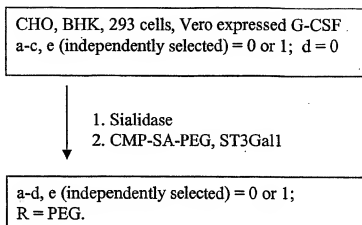


FIG. 29B

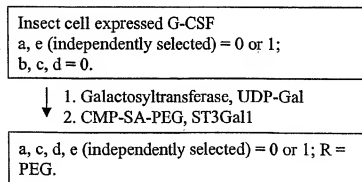


FIG. 29C

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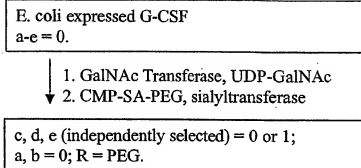


FIG. 29D

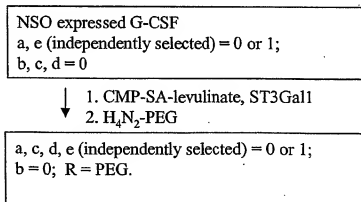


FIG. 29E

63/498

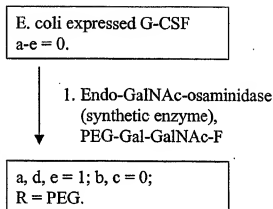


FIG. 29F

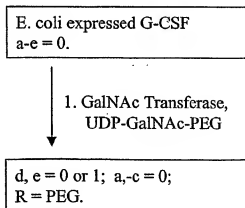
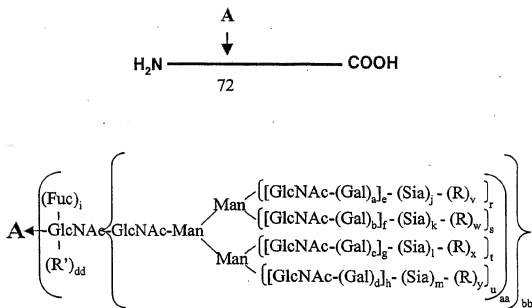


FIG. 29G

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a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 30A

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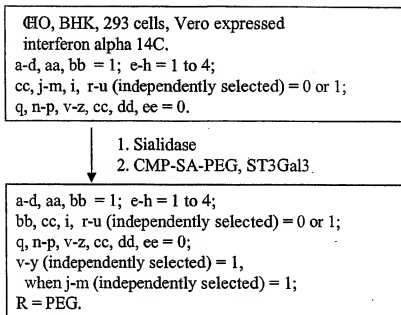


FIG. 30B

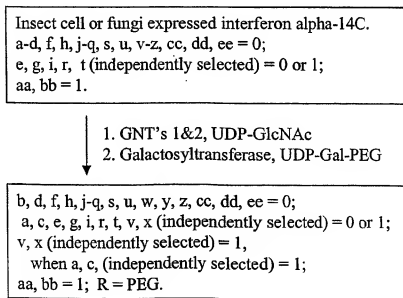


FIG. 30C

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Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

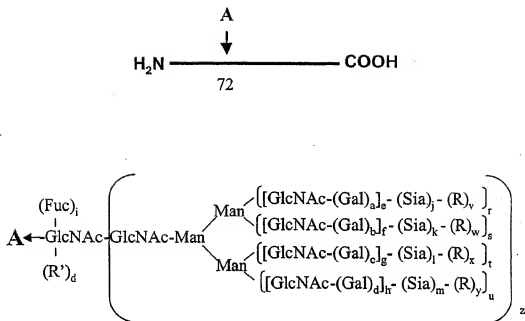
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 30D

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 30E

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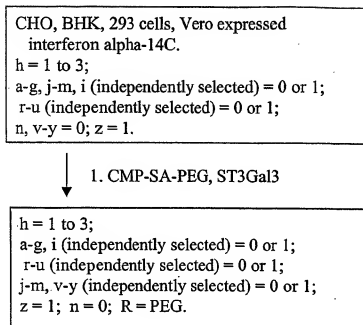


FIG. 30F

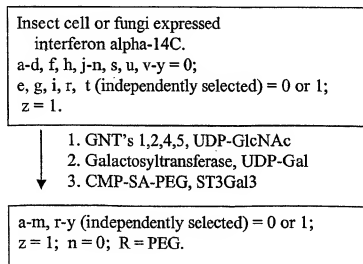


FIG. 30G

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Yeast expressed interferon alpha-14C.
 a-n = 0; r-y (independently selected) = 0 to 1;
 z = 1; R (branched or linear) = Man,
 oligomannose.

1. mannosidases
2. GNT's 1,2,4,5, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal
- 4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 30H

NSO expressed interferon alpha 14C.
 a-i, r-u (independently selected) = 0 or 1;
 j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;
 n = 0; z = 1; R = PEG.

FIG. 30I

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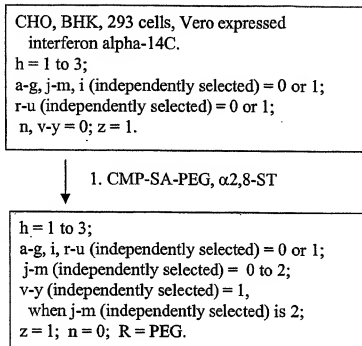


FIG. 30J

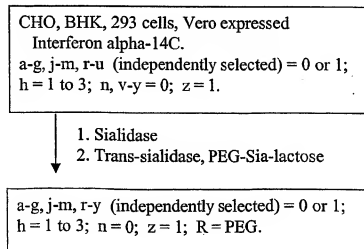


FIG. 30K

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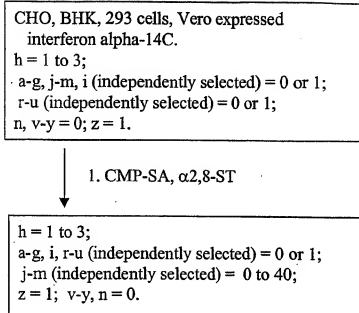


FIG. 30L

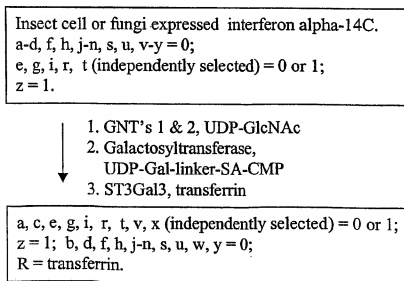


FIG. 30M

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Insect cell or fungi expressed interferon alpha-14C.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
 2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
 3. ST3Gal3, transferrin

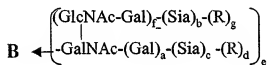
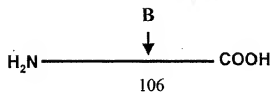
i (independently selected) = 0 or 1;

a-h, j-m, r-z = 0;

n = 1; R' = -Gal-linker-transferrin.

FIG. 30N

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a-c, e, f (independently selected) = 0 or 1;
 d, g = 0; R = polymer, glycoconjugate.

FIG. 300

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CHO, BHK, 293 cells, Vero expressed
IF-alpha (2a or 2b).
a-c (independently selected) = 0 or 1;
e = 1; d, f, g = 0

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal1

a-d (independently selected) = 0 or 1;
e = 1; b, f, g = 0; R = PEG.

FIG. 30P

Insect cell expressed interferon alpha (2a or 2b).
a, e (independently selected) = 0 or 1;
b, c, d, f, g = 0.

- ↓
1. Galactosyltransferase, UDP-Gal
 2. CMP-SA-PEG, ST3Gal1

a, c, d, e (independently selected) = 0 or 1;
b, f, g = 0; R = PEG.

FIG. 30Q

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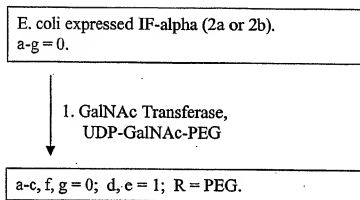


FIG. 30R

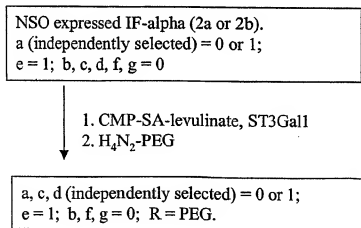


FIG. 30S

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E. coli expressed IF-alpha (2a or 2b).
a-g = 0.



1. Endo-N-acetylgalactosamidase
(synthetic enzyme),
PEG-Gal-GalNAc-F

a, d, e = 1; b, c, f, g = 0; R = PEG.

FIG. 30T

E. coli expressed IF-alpha (2a or 2b).
a-g = 0.



1. GalNAc Transferase, UDP-GalNAc
2. sialyltransferase, CMP-SA-PEG

b, d = 0 or 1; e = 1; a, c, f, g = 0; R = PEG.

FIG. 30U

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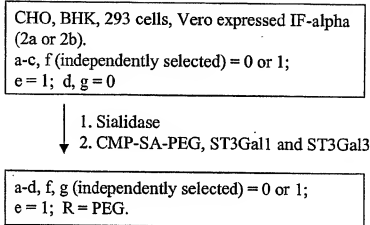


FIG. 30V

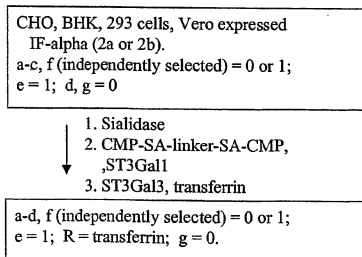
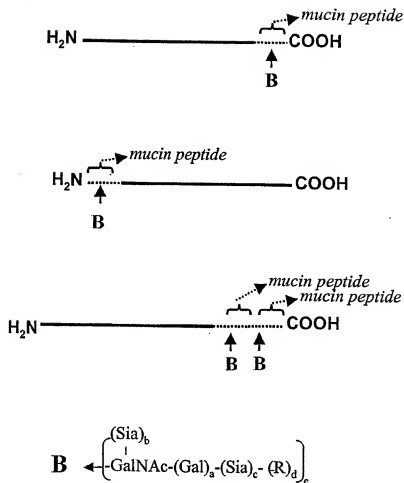


FIG. 30W

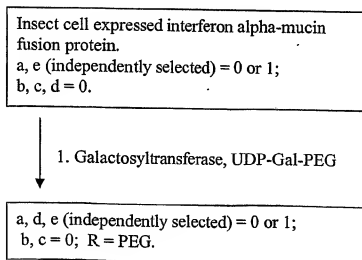
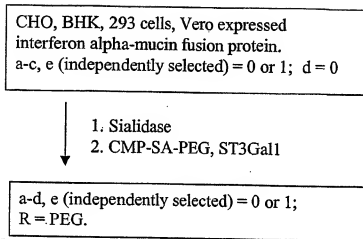
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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer, glycoconjugate.

FIG. 30X

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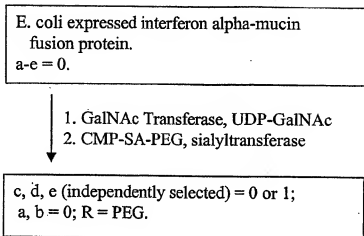
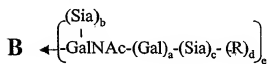
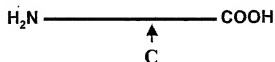
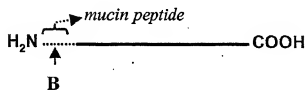
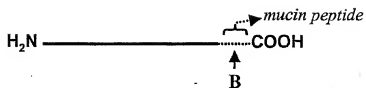


FIG. 30AA

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a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 30BB

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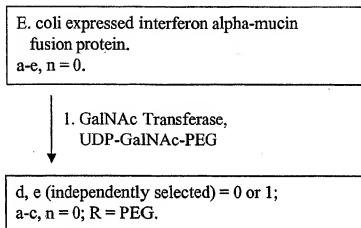


FIG. 30CC

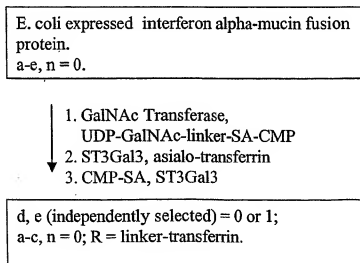


FIG. 30DD

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E. coli expressed Interferon alpha (no fusion).
a-e, n = 0.

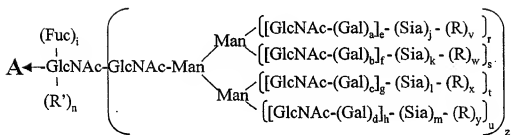
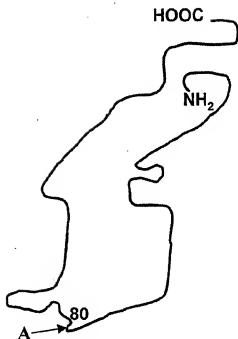


1. NHS-CO-linker-SA-CMP
2. ST3Gal3, transferrin

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 30EE

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 31A

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CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31B

Insect cell expressed IF-beta
 a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0 or 1;
 z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3,
buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 z = 1; R = PEG.

FIG. 31C

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Yeast expressed IF-beta
 a-n = 0; z = 1;
 r-y (independently selected) = 0 to 1;
 R (branched or linear) = Man, oligomannose or
 polysaccharide.

- ↓ 1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed IF-beta
 h = 1 to 3;
 a-g, j-m, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1.

- ↓ 1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;
 a-g, i (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 31E

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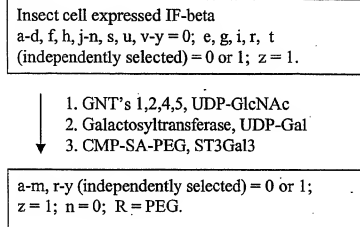


FIG. 31F

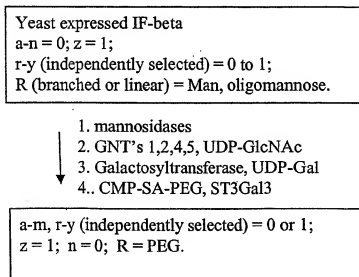


FIG. 31G

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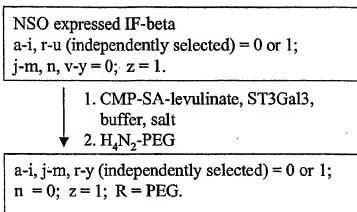


FIG. 31H

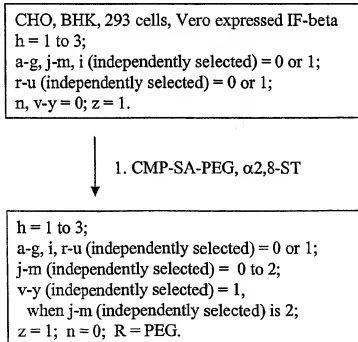


FIG. 31I

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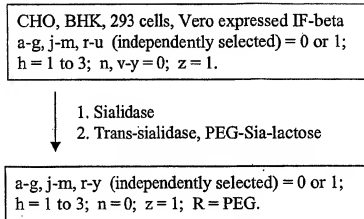


FIG. 31J

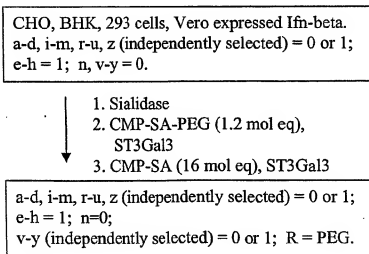


FIG. 31K

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NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,
when j-m (independently selected) is 1;

FIG. 31L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 31M

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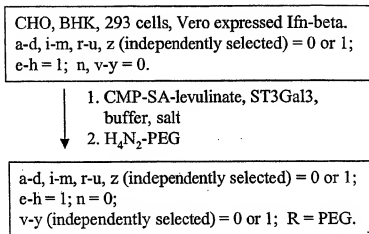


FIG. 31N

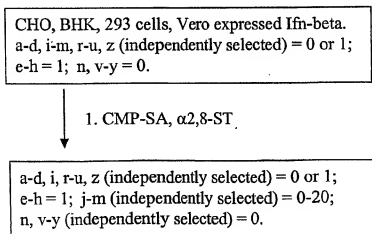


FIG. 31O

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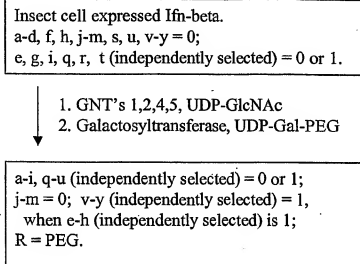


FIG. 31Q

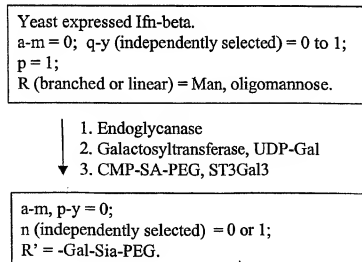


FIG. 31R

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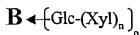
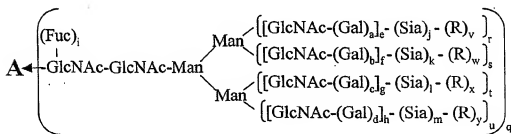
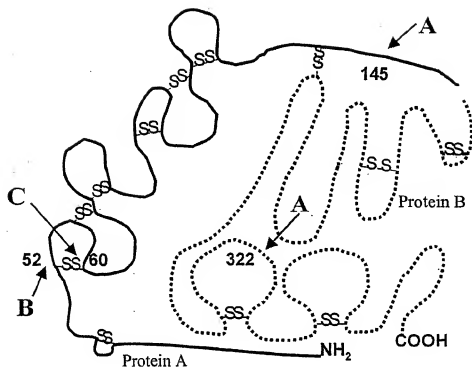
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 31S

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a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 32A

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BHK expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mole eq),
ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
v, x, (independently selected) = 1,
when j, l (respectively, independently selected) is 1;
R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mole eq),
ST3Gal3
 3. CMP-SA (8 mol eq), ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
v or x, (independently selected) = 1,
when j or l, (respectively, independently selected) is 1;
R = PEG.

FIG. 32C

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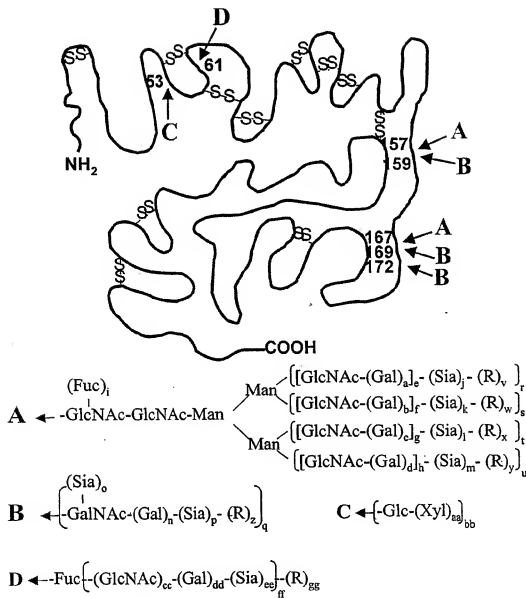
NSO expressed Factor VII or VIIa
a--u (independently selected) = 0 or 1;
v-y = 0; n = 0-4;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;
n = 0-4; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
Sia = Sia; R = PEG.

FIG. 32D

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a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 33A

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 R = PEG.

FIG. 33B

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3
 3. ST3Gal1, CMP-SA

a-d, n, p, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 o, z = 0; R = PEG.

FIG. 33C

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

- ↓
1. sialidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA, ST3Gal3
 4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1; R = PEG;
 o, v-y, gg = 0;
 j-m, p, ee (independently selected) = 0 or 1, but when
 p = 1, z = 1.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
- CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1; R = PEG;
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =
 0 or 1.

FIG. 33E

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CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 33F

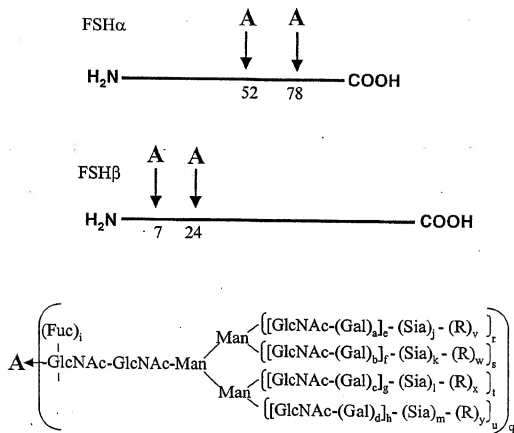
CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1;
 e-h, aa = 1 to 4;
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG, α 2,8-ST

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee (independently selected) = 0 to 2;
 v-y, gg (independently selected) = 1, when j-m
 (independently selected) is 2;

FIG. 33G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 34A

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CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 34B

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 34C

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NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 34E

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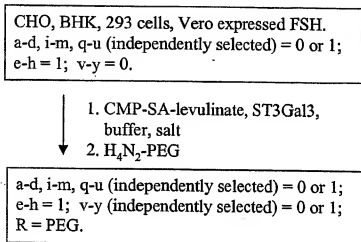


FIG. 34F

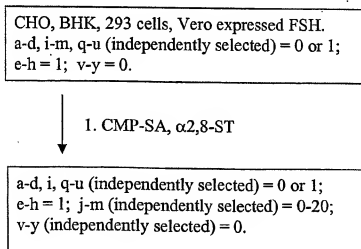


FIG. 34G

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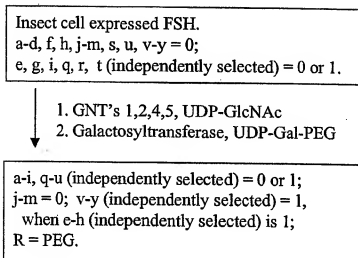


FIG. 34H

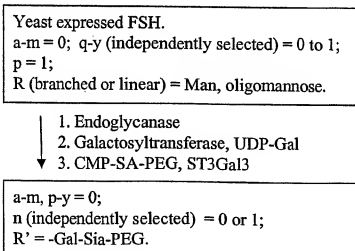


FIG. 34I

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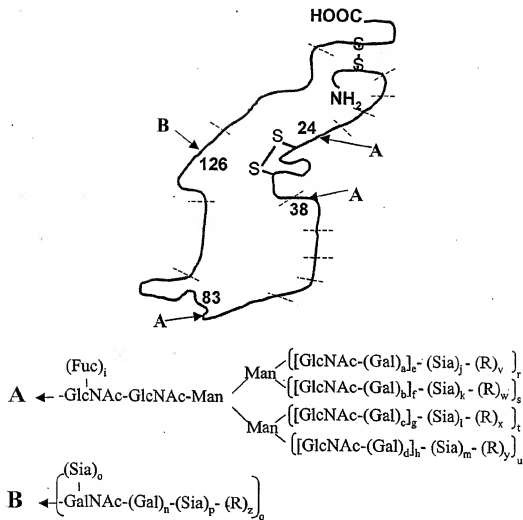
CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated chorionic gonadotrophin (CG) produced in CHO.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-CG.

FIG. 34J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35A

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CHO, BHK, 293 cells, Vero expressed EPO
 a-g, n, q = 1; h = 1 to 3;
 j-m, i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; v-z = 0

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
 i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 j-m, v-y (independently selected) = 0 or 1;
 R = PEG; z = 0.

FIG. 35B

Insect cell expressed EPO
 a-d, f, h, j-q, s, u, v-z = 0;
 e, g, i, r, t (independently selected) = 0 or 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 2. CMP-SA-PEG, ST3Gal3

b, d, f, h, k, m-q, s, u, w, y, z = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 j, l, v, x (independently selected) = 0 or 1;
 R = PEG.

FIG. 35C

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CHO, BHK, 293 cells, Vero expressed EPO
 a-q, r-u (independently selected) = 0 or 1;
 v-z = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
- ↓ 4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;
 i-m, o, r-u (independently selected) = 0 or 1;
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed EPO
 a-g, n, q = 1; h = 1 to 3;
 j-m, i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 v-z = 0

- ↓ 1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
 i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1;
 j-m, v-y (independently selected) = 0 or 1;
 R = PEG; z = 0.

FIG. 35E

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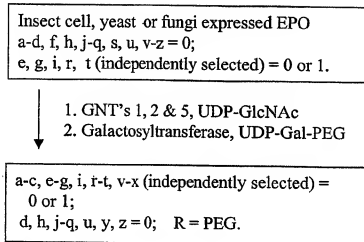


FIG. 35F

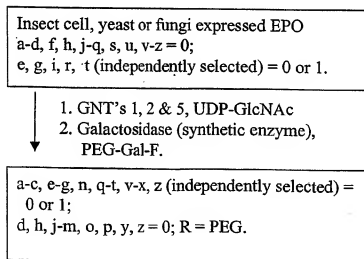


FIG. 35G

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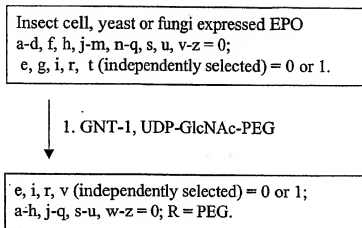


FIG. 35H

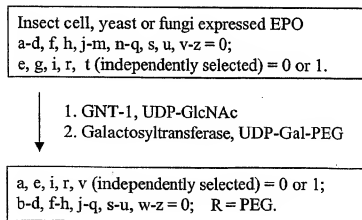


FIG. 35I

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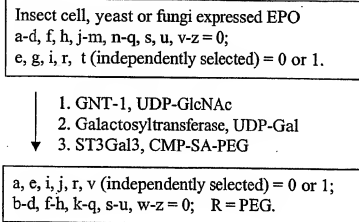


FIG. 35J

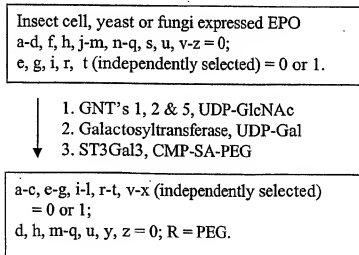


FIG. 35K

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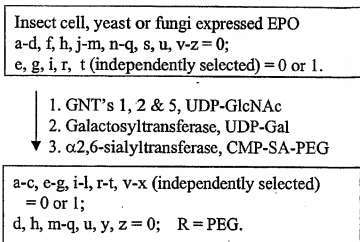


FIG. 35L

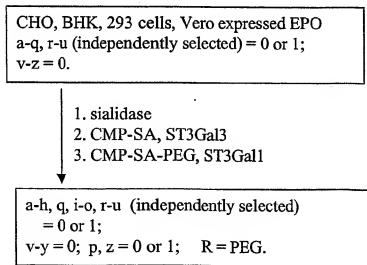


FIG. 35M

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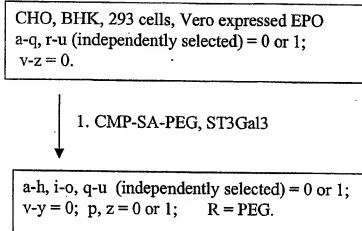


FIG. 35N

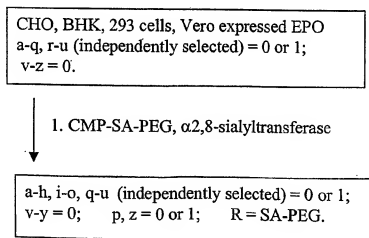


FIG. 35O

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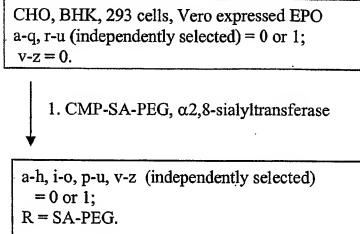


FIG. 35P

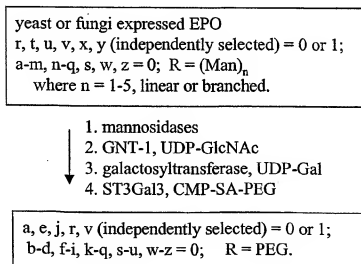


FIG. 35Q

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yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 a-m, n-q, s, w, z = 0; $R = (\text{Man})_n$
 where n = 1-5, linear or branched.

- ↓
 1. mannosidases
 2. GNT-1, UDP-GlcNAc-PEG

c, r, v (independently selected) = 0 or 1;
 a-h, i-q, s-u, w-z = 0; $R = \text{PEG}$.

FIG. 35R

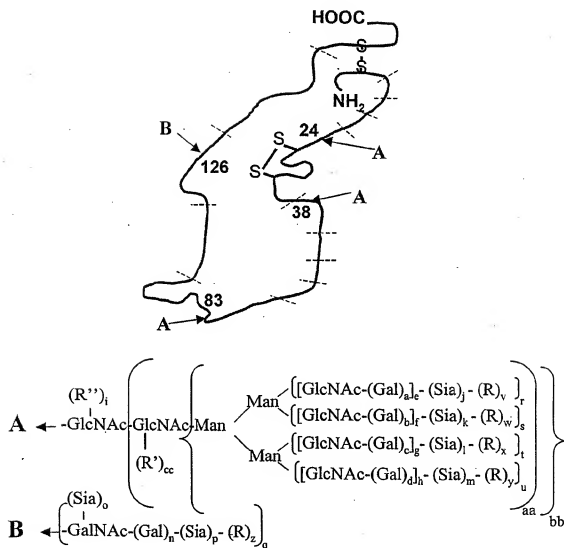
yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 a-m, n-q, s, w, z = 0; $R = (\text{Man})_n$
 where n = 1-5, linear or branched.

- ↓
 1. mannosidase-I
 2. GNT-1, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal
 4. ST3Gal3, CMP-SA-PEG

a, c, j, r, t-u, v, x, y (independently selected)
 = 0 or 1;
 b-d, f-i, k-q, s, w, z = 0;
 $(R)_v = \text{PEG}$; $(R)_x$ and $(R)_y = \text{Man}$.

FIG. 35S

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; aa, bb = 1; cc = 0;

R = polymer; R'' and R' = sugar-polymer or Fuc.

FIG. 35T

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yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 cc, a-m, n-q, s, w, z = 0;
 aa, bb = 1;
 $R = (\text{Man})_n$ where $n = 1-100$, linear or branched.

- ↓
 1. endo-H
 2. galactosyltransferase, UDP-Gal-PEG

i (independently selected) = 0 or 1;
 aa, bb, cc, a-h, j-z = 0; $R'' = \text{Gal-PEG}$.

FIG. 35U

yeast or fungi expressed EPO
 r, t, u, v, x, y (independently selected) = 0 or 1;
 cc, a-m, n-q, s, w, z = 0; aa, bb = 1;
 $R = (\text{Man})_n$ where $n = 1-100$, linear or branched.

- ↓
 1. endo-H
 2. galactosyltransferase, UDP-Gal
 3. ST3Gal3, CMP-SA-PEG

i (independently selected) = 0 or 1;
 aa, bb, cc, a-h, j-z = 0; $R'' = \text{Gal-SA-PEG}$.

FIG. 35V

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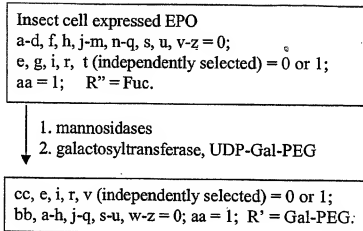


FIG. 35W

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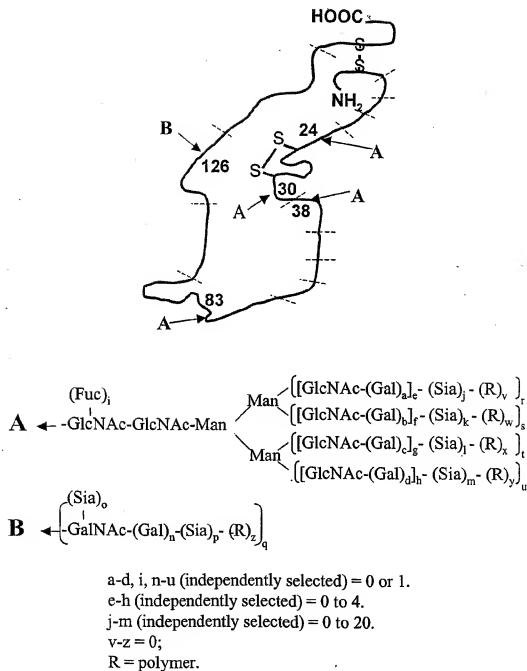


FIG. 35X

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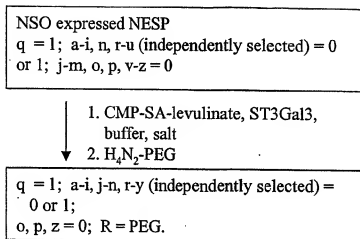


FIG. 35Y

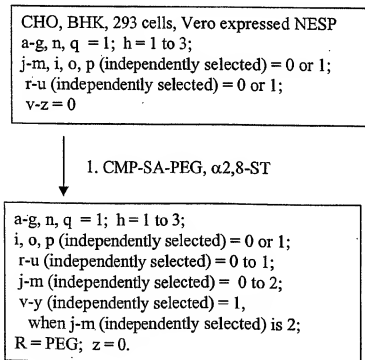


FIG. 35Z

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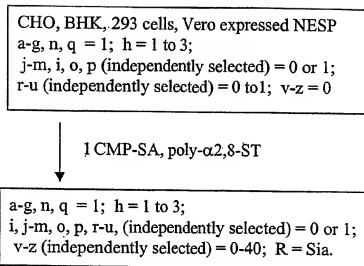
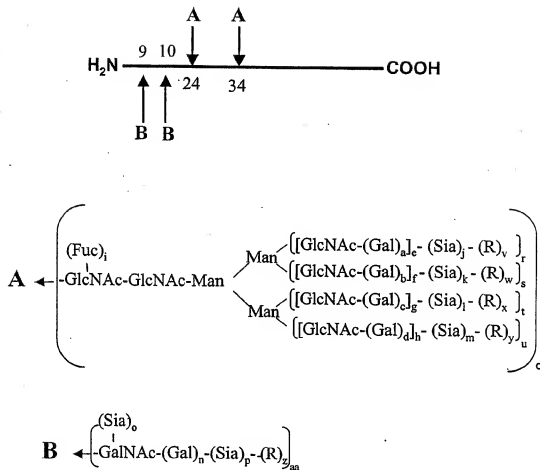


FIG. 35AA

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a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 36A

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
o, p, z = 0; n, e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 36B

CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3 &
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;
o, z = 0; n, e-h = 1;
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 36C

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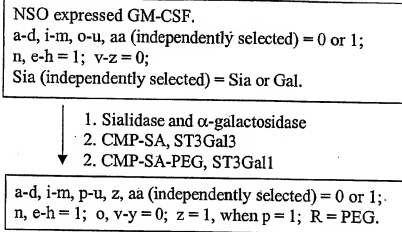


FIG. 36D

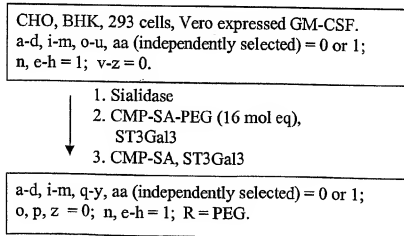


FIG. 36E

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CHO, BHK, 293 cells, Vero expressed GM-CSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;
z = 0; n, e-h = 1; R = PEG.

FIG. 36F

CHO, BHK, 293 cells, Vero expressed GMCSF.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

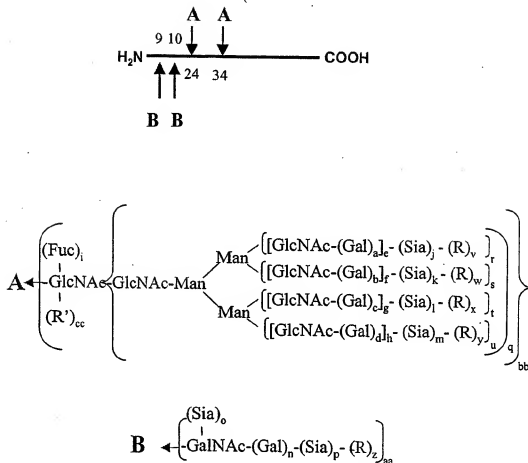


1. CMP-SA, α 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; j-m (independently selected) = 0-20;
v-z (independently selected) = 0.

FIG. 36G

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a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

c-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

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Insect cell expressed GM-CSF.

a-d, f, h, j-m, o, p, s, u, v-z = 0;

c, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 36I

Yeast expressed GM-CSF.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. Endoglycanase
2. mannosidase (if aa = 1).
3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;

q, cc (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 36J

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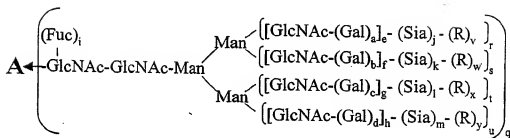
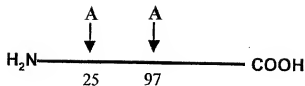
CHO, BHK, 293 cells, Vero expressed GM-CSF.
a--m, o-u, aa, bb (independently selected) = 0 or 1;
n, v-z, cc = 0.

- ↓
1. sialidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-linker-SA-CMP, ST3Gal1
 3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 36K

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 37A

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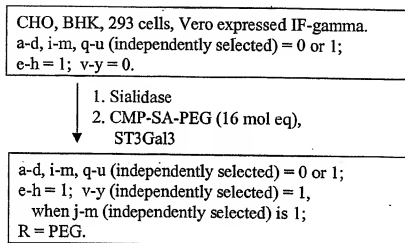


FIG. 37B

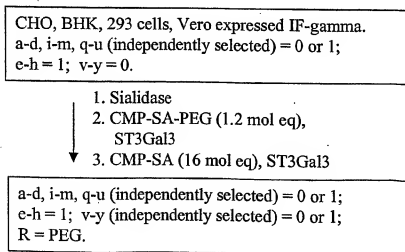


FIG. 37C

133/498

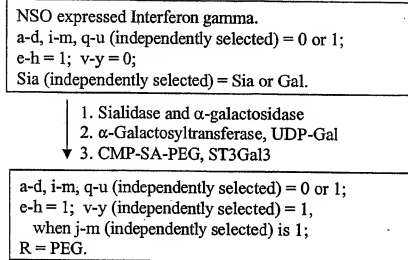


FIG. 37D

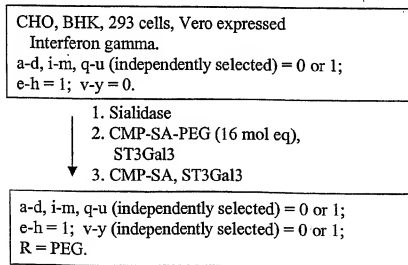


FIG. 37E

134/498

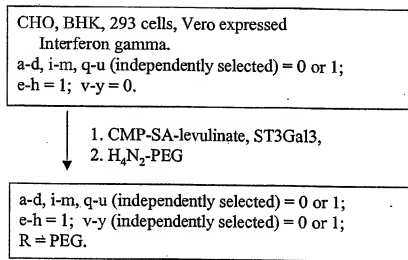


FIG. 37F

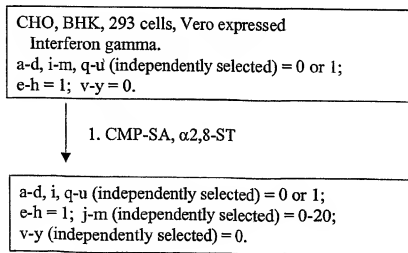
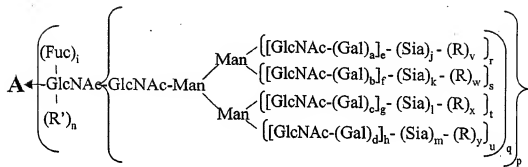
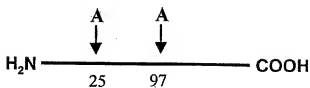


FIG. 37G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 37H

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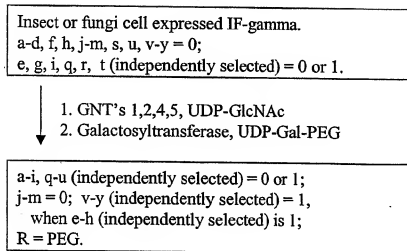


FIG. 37I

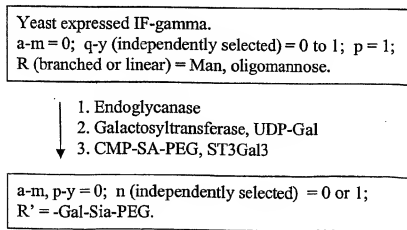


FIG. 37J

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CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP, ST3Gal3
 2. Galactosyltransferase, transferrin treated with endoglycanase.

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 37K

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1; n, v-y = 0.

- ↓
1. CMP-SA-PEG,
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h, p = 1;
n, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 37L

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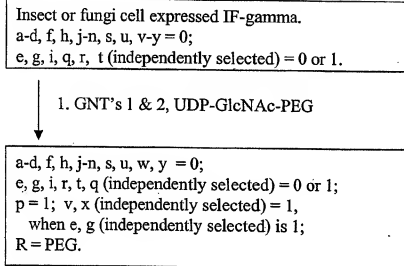


FIG. 37M

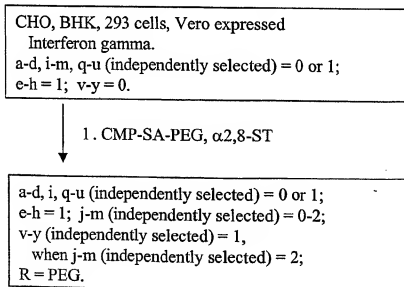
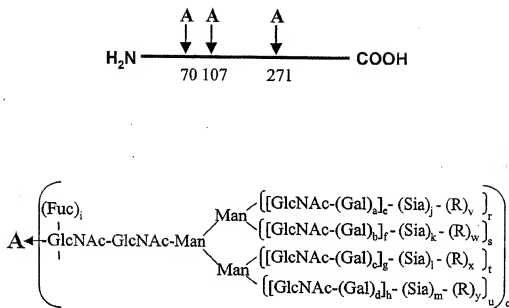


FIG. 37N

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 38A

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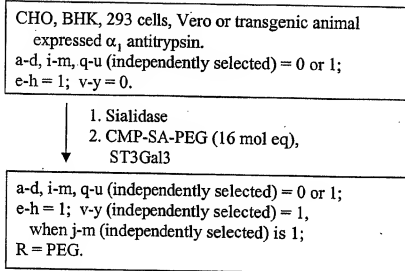


FIG. 38B

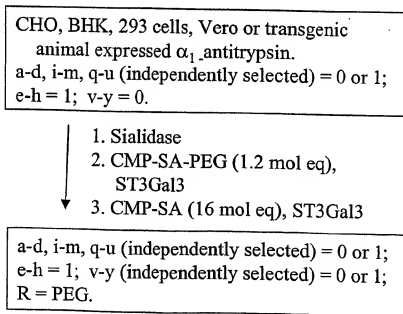


FIG. 38C

141/498

CHO, BHK, 293 cells, Vero or transgenic animal
expressed alpha-1 antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38D

CHO, BHK, 293 cells, Vero or transgenic animal
expressed α_1 -antitrypsin.

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38E

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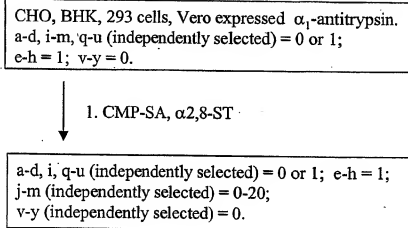
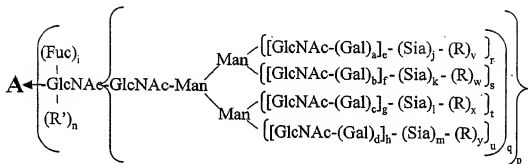
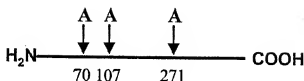


FIG. 38F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 38G

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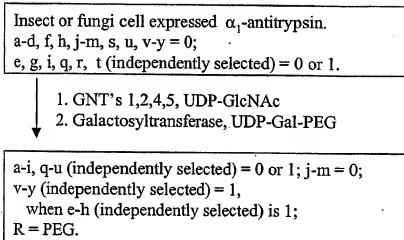


FIG. 38H

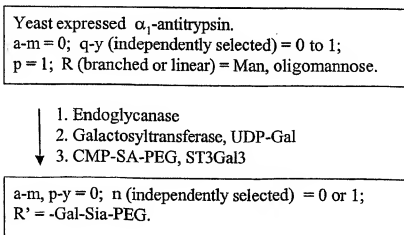


FIG. 38I

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CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

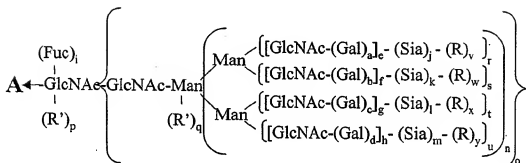
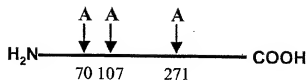


1. CMP-SA-linker-Gal-UDP,
ST3Gal3
2. Galactosyltransferase, transferrin treated
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 38J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 38K

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Yeast expressed alpha-1 antitrypsin.

a-h, i-m, p, q = 0;

R (independently selected) = mannose, oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1; n, o = 1.

↓ 1. endoglycanase

▼ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 38L

Plant expressed alpha-1 antitrypsin.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n = 1; R' = xylose

↓ 1. hexosaminidase,

2. alpha mannosidase and xylosidase

▼ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 38M

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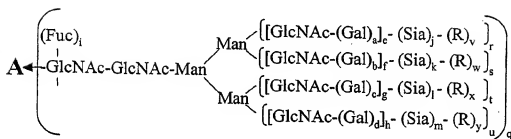
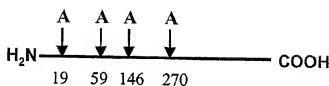
CHO, BHK, 293 cells, Vero, transgenic animal
expressed α_1 antitrypsin.
a-h, i-o, r-u (independently selected) = 0 or 1;
p, q, v-y = 0.

↓
1. CMP-SA-PEG,
ST3Gal3

a-h, i-o, r-u (independently selected) = 0 or 1;
p, q = 0; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 38N

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 39A

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CHO, BHK, 293 cells, Vero expressed Cerezyme
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 39B

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-M-6-P (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = mannose-6-phosphate

FIG. 39C

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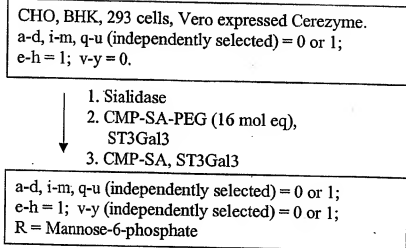


FIG. 39D

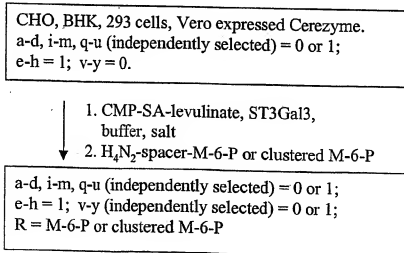


FIG. 39E

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CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 39F

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Insect cell expressed Cerezyme.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 39H

Yeast expressed Cerezyme.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 39I

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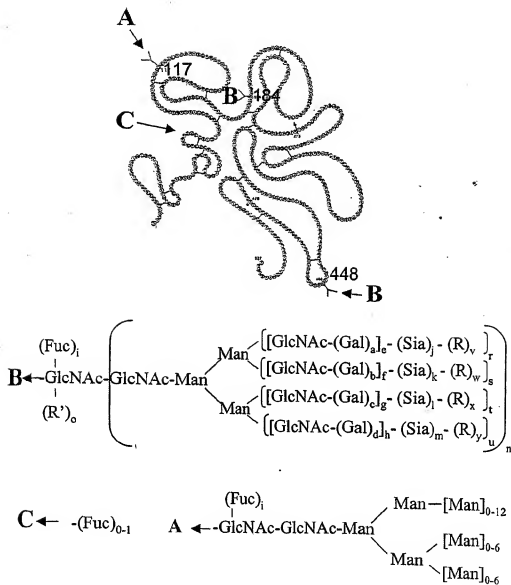
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0; v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 39J

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a-d, i, n-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 4.
 j-m (independently selected) = 0 to 20.
 R = polymer; R' = sugar, glycoconjugate.

FIG. 40A

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CHO, BHK, 293 cells, Vero expressed tPA
 a-g, n = 1; h = 1 to 3;
 j-m, i, (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
- ▼ 4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;
 i, r-u (independently selected) = 0 or 1;
 o = 0; j-m, v-y (independently selected) = 0 or 1;
 R = PEG

FIG. 40B

Insect or fungi cell expressed tPA
 A = B; a-d, f, h, j-o, s, u, v-y = 0;
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
- ▼ 3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 n = 1; j, l, v, x (independently selected) = 0 or 1;
 R = PEG.

FIG. 40C

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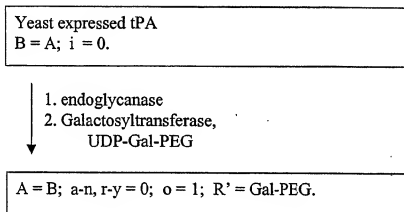


FIG. 40D

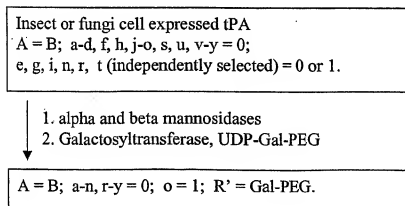


FIG. 40E

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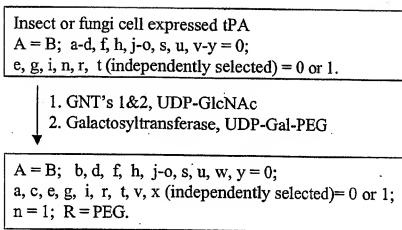


FIG. 40F

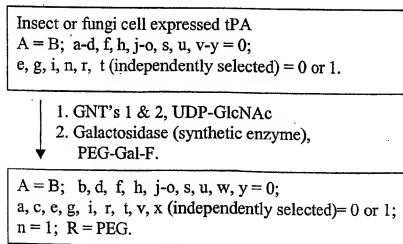
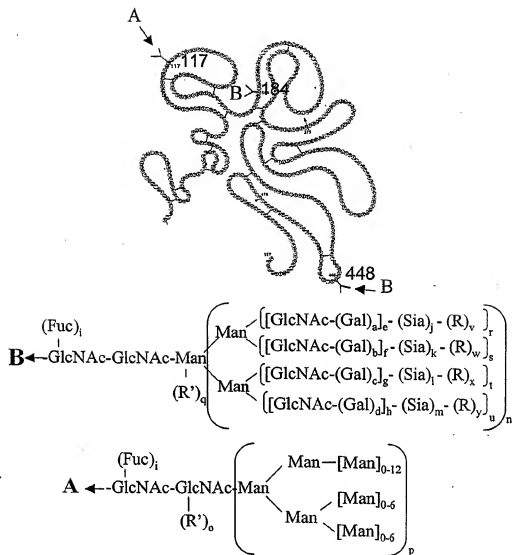


FIG. 40G

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40H

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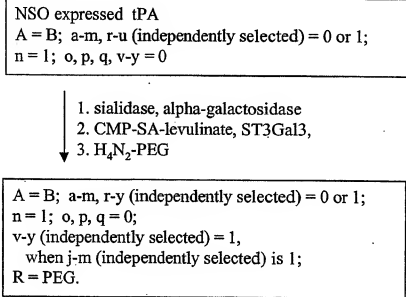


FIG. 40I

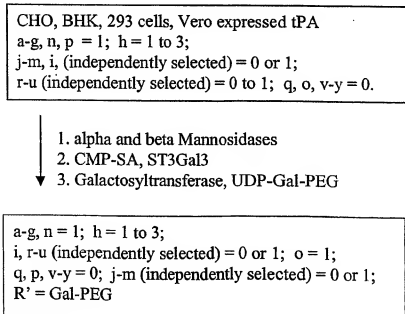


FIG. 40J

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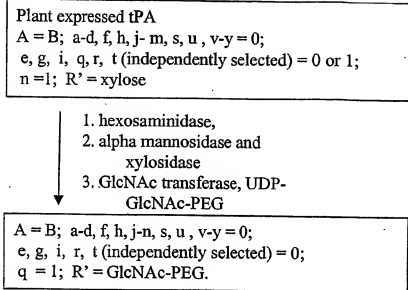


FIG. 40K

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 40M

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40N

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NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

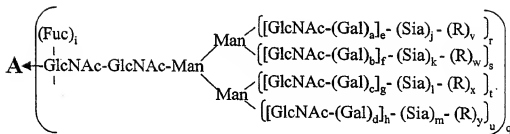
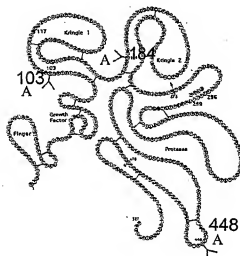
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 400

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40P

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CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40Q

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 40R

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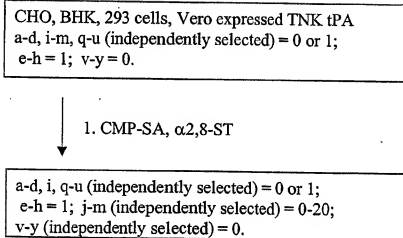
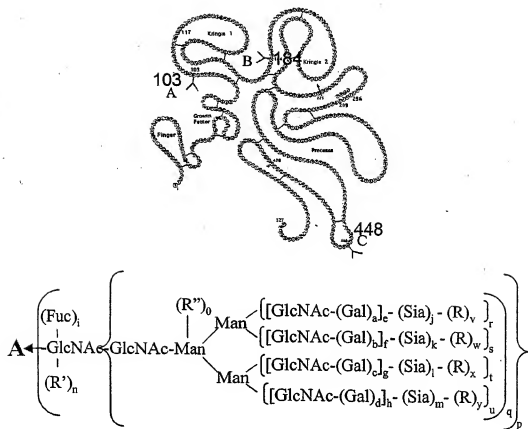


FIG. 40S

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a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 40T

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Insect cell expressed TNK tPA

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 40U

Yeast expressed TNK tPA

a-m = 0; q-y (independently selected) = 0 to 1; p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 40V

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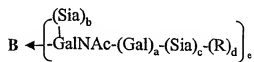
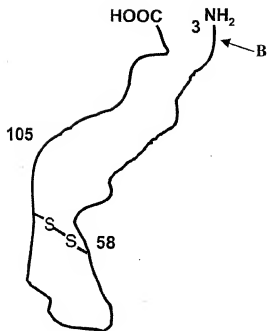
CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, anti-TNF
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;
n = 0; v-y (independently selected) = 0 or 1;
R = linker-anti-TNF IG chimera protein.

FIG. 40W

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a-c, e (independently selected) = 0 or 1;
 d = 0;
 R = modifying group, mannose, oligo-
 mannose.

FIG. 41A

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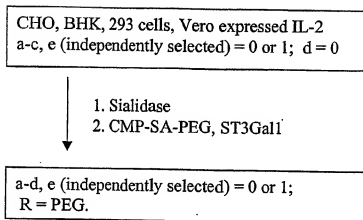


FIG. 41B

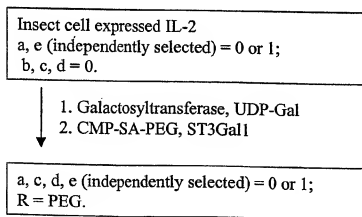


FIG. 41C

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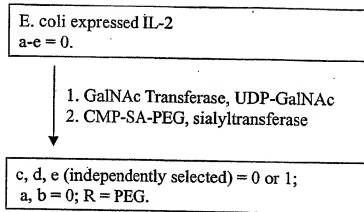


FIG. 41D

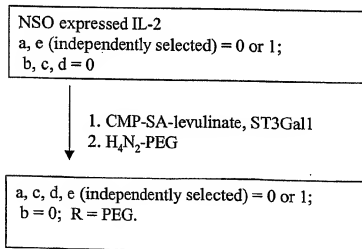


FIG. 41E

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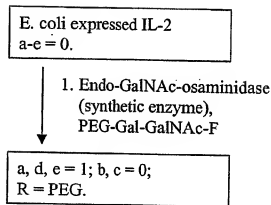


FIG. 41F

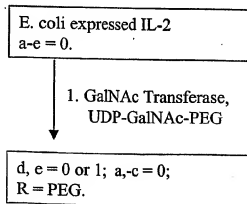
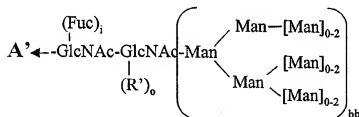
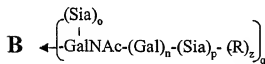
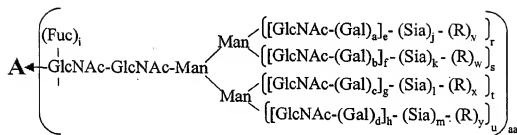


FIG. 41G

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2 peptides
 A and A' - N-linked sites
 B - O-linked sites



Alternate structure
 for some N-linked
 structures of A.

a-d, i, n-u (independently selected) = 0 or 1.
 aa, bb (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 20.
 v-z = 0; R = polymer, glycoconjugate.

FIG. 42A

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CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3
 3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42C

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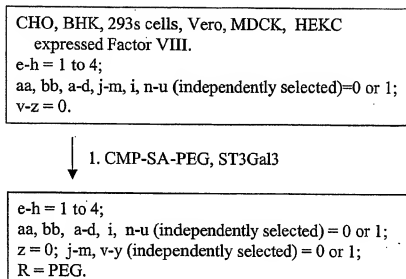


FIG. 42D

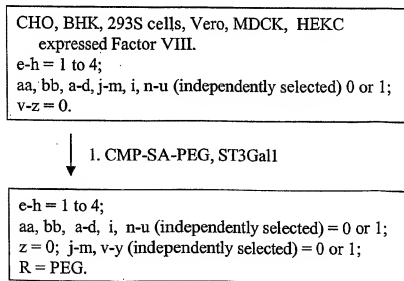


FIG. 42E

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;
v-z = 0.



1. CMP-SA-PEG, α 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

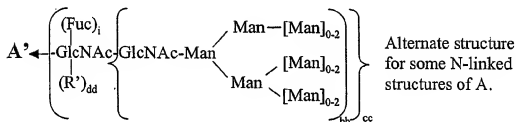
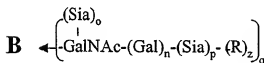
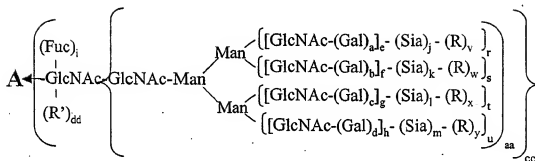
when j-m (independently selected) is 2;

R = PEG.

FIG. 42F

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2 peptides

A or A' - N-linked sites**B** - O-linked sites

a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 42G

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
 2. H₄N₂-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;
dd, z = 0; j-m, v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42H

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. endo-H
 2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;
cc, v-z = 0; R' = -Gal-PEG.

FIG. 42I

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
 2. endo-H
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;
cc, v-z = 0; R' = -Gal-PEG.

FIG. 42J

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

- ↓
1. mannosidases
 2. GNT 1 & 2, UDP-GlcNAc
 3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;
bb, cc, dd, z = 0; R = PEG.

FIG. 42K

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CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

1. mannosidases
- ↓ 2. GNT-1, 2, 4 & 5; UDP-GlcNAc
3. galactosyltransferase, UDP-Gal
4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;
dd, v-z = 0.

FIG. 42L

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;
dd, v-z = 0.

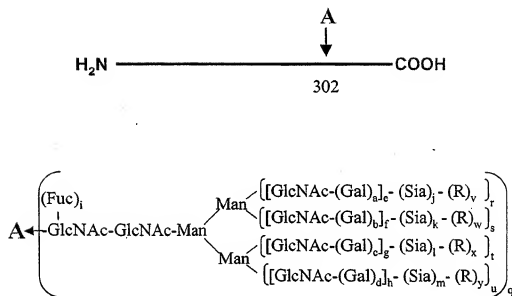
- ↓ 1. mannosidases
2. GNT-1, UDP-GlcNAc-PEG

e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;
bb, cc, dd, z = 0.

FIG. 42M

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 43A

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CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 43B

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 43C

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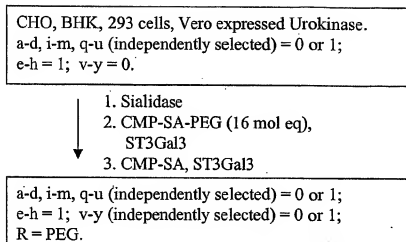


FIG. 43D

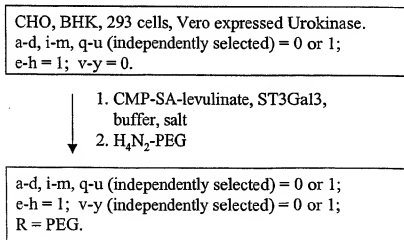


FIG. 43E

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CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

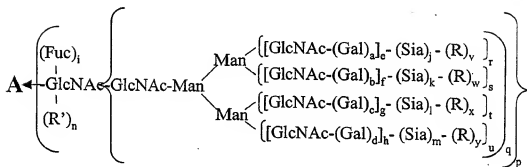
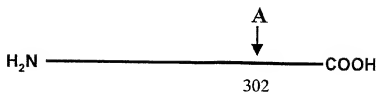


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 43F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 43G

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Insect cell expressed Urokinase.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-n = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 43H

Yeast expressed Urokinase.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 43I

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CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated Urokinase produced in CHO.
 - ↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 43J

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase
 2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 43K

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Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase, hexosaminidase
 2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 43L

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44C

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq), ST3Gal3
3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44D

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.



1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 44E

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CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

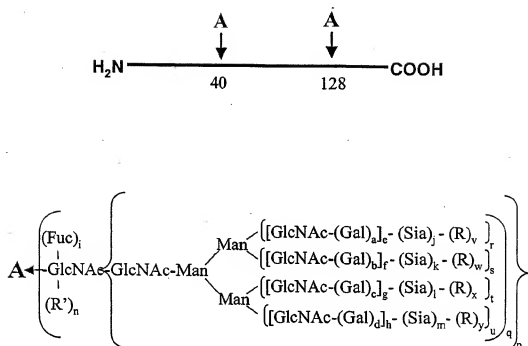


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 44F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 44G

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Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 44H

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 44I

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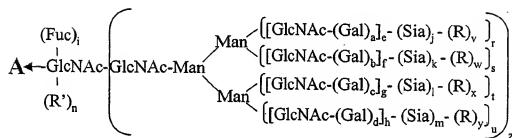
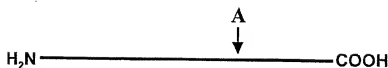
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker- alpha-1-Proteinase inhibitor.

FIG. 44J

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 45A

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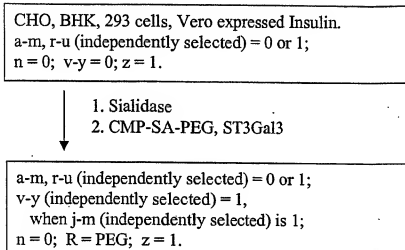


FIG. 45B

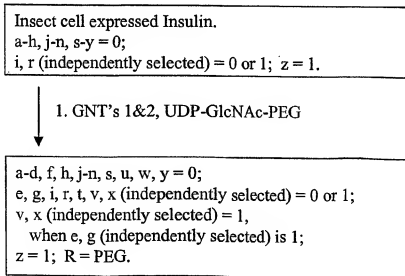


FIG. 45C

201/498

Yeast expressed Insulin.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.



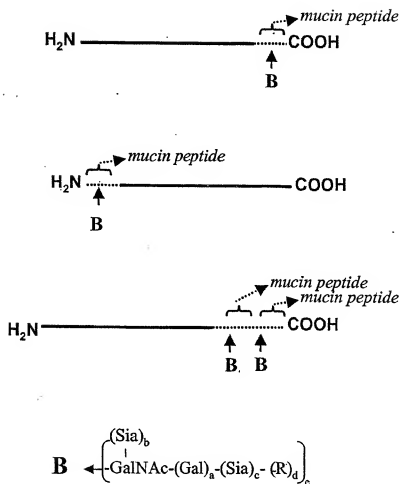
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 45D

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 45E

203/498

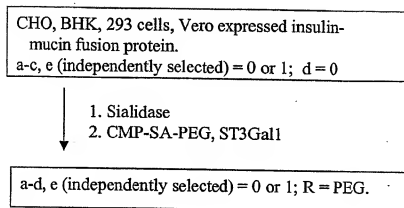


FIG. 45F

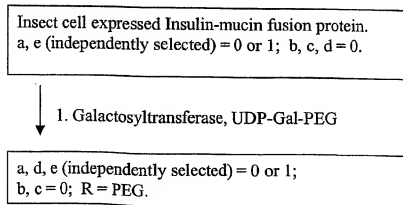


FIG. 45G

204/498

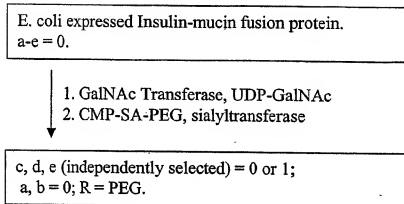
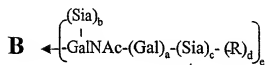
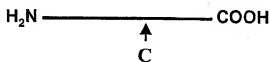
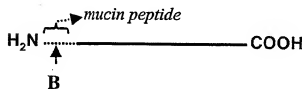
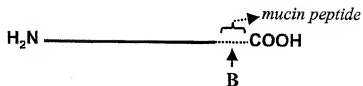


FIG. 45H

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = modifying group, mannose,
 oligo-mannose.

FIG. 45I

206/498

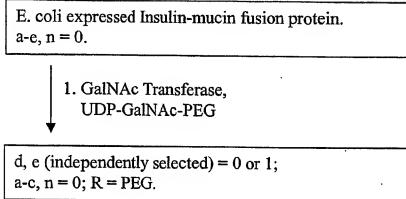


FIG. 45J

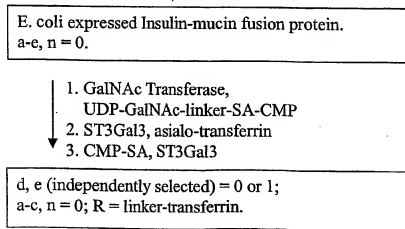


FIG. 45K

207/498

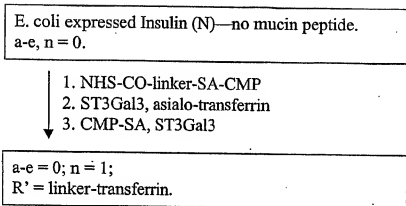
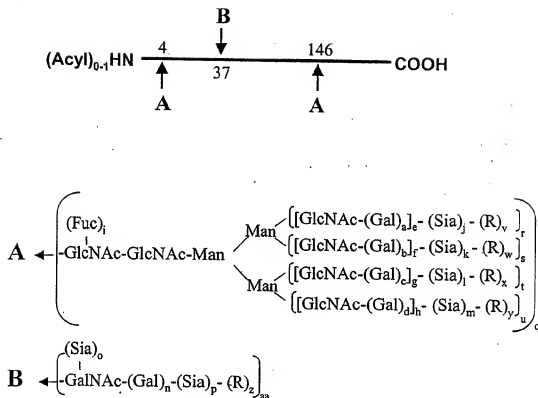


FIG. 45L

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a-d, i, n-u, aa (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer, glycoconjugate.

FIG. 46A

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CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-linker-lipid-A,
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
o, p, z = 0; n, e-h = 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = linker-lipid-A.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed M-antigen.
a-d, i-m, o-u, aa (independently selected) = 0 or 1;
n, e-h = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-linker-tetanus toxin, ST3Gal1
 3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 46C

210/498

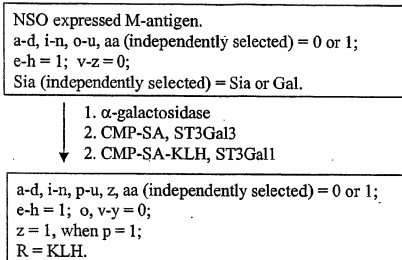


FIG. 46D

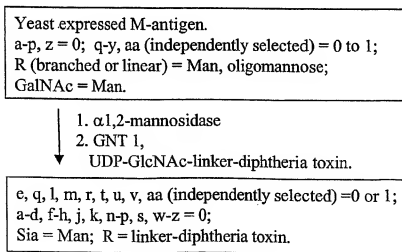


FIG. 46E

211/498

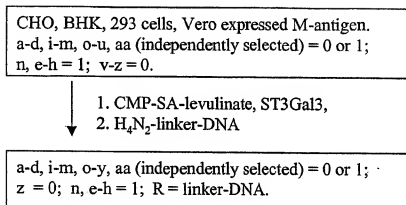


FIG. 46F

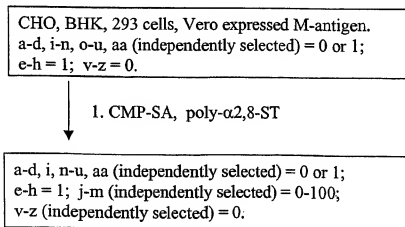


FIG. 46G

213/498

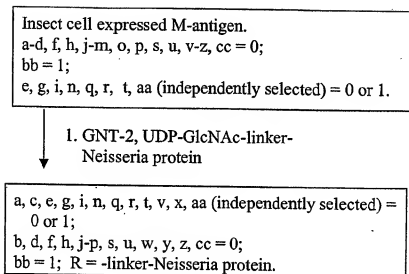


FIG. 46I

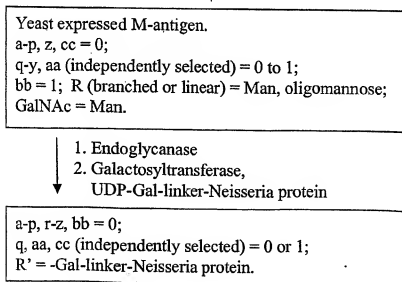


FIG. 46J

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Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. mannosidases

2. GNT 1 & 2, UDP-GlcNAc

3. UDP-Gal, Galactosyltransferase,

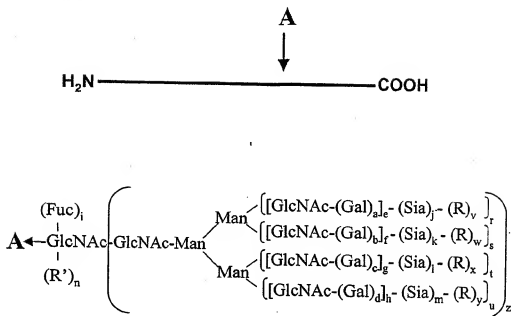
4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 46K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 47A

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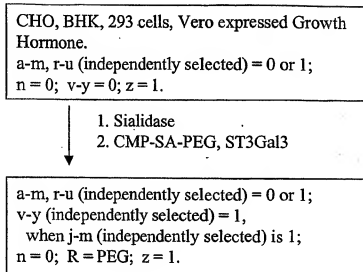


FIG. 47B

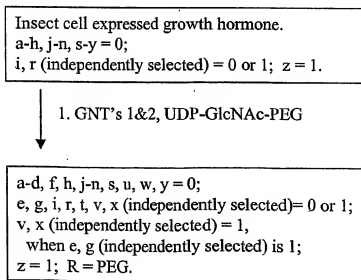


FIG. 47C

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Yeast expressed growth hormone.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

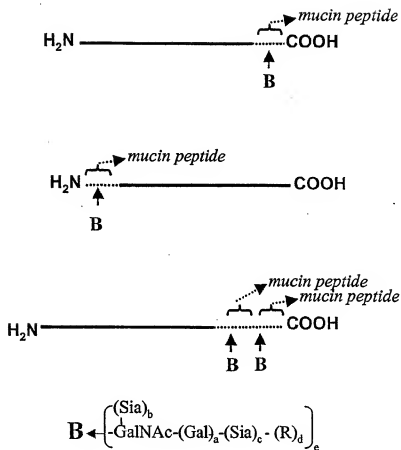
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z = 0; n = 1; R' = -Gal-PEG.

FIG. 47D

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 47E

219/498

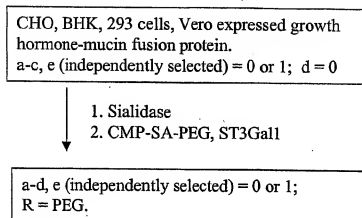


FIG. 47F

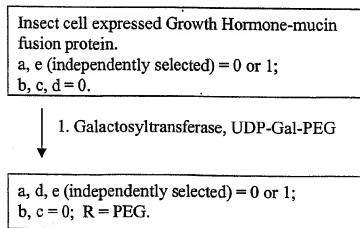


FIG. 47G

220/498

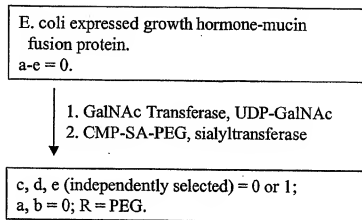


FIG. 47H

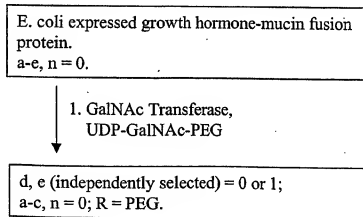


FIG. 47I

221/498

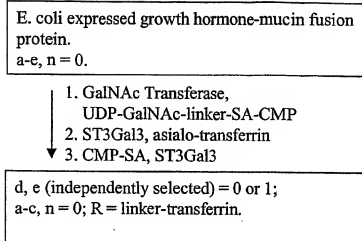


FIG. 47J

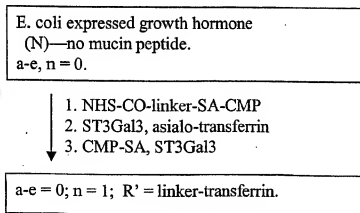
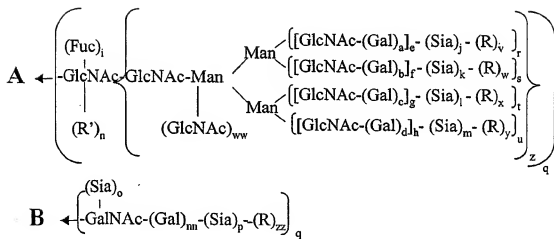
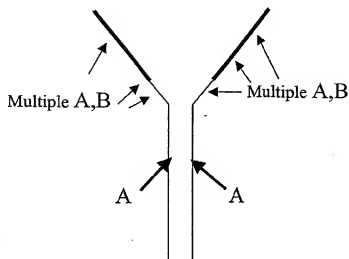


FIG. 47K

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a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

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CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
 2. galactosyltransferase, UPD-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 48C

224/498

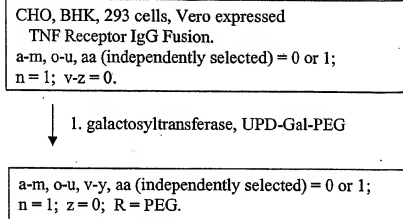


FIG. 48D

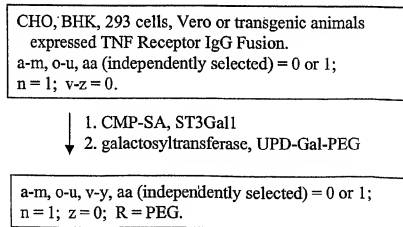


FIG. 48E

225/498

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal1
2. H₄N₂-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 48F

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA-PEG, α 2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;
n = 1; j-m, p (independently selected) = 0 to 2;
v-z (independently selected) = 1,
when j-m, p (independently selected) is 2;
R = PEG.

FIG. 48G

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CHO, BHK, 293 cells, Vero expressed Herceptin.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.

- ↓
 1. galactosyltransferase, UPD-Gal
 2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
 e, g, r, t = 1; R = toxin;
 f, h, k, m, n, s, u-y = 0; q, z = 1;
 v-y (independently selected) = 51,
 when j, l (independently selected) is 1.

FIG. 49B

CHO, BHK, 293 cells, Vero or fungal expressed Herceptin.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.

- ↓
 1. galactosyltransferase,
 UPD-Gal-Toxin

a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when a, c (independently selected) is 1;
 R = toxin.

FIG. 49C

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Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

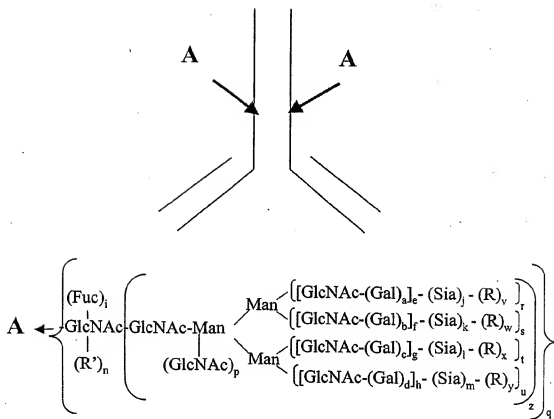
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

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a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 50A

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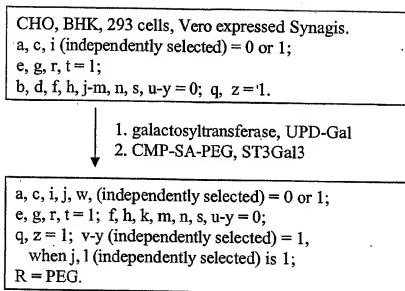


FIG. 50B

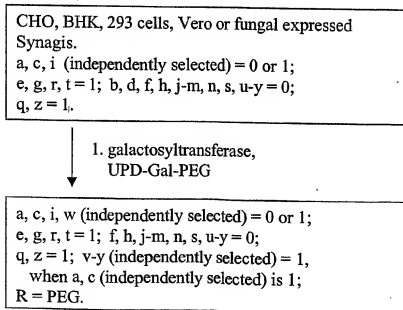


FIG. 50C

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Fungi expressed Synagis.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

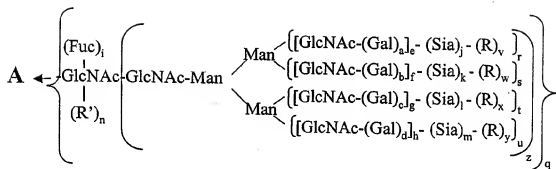
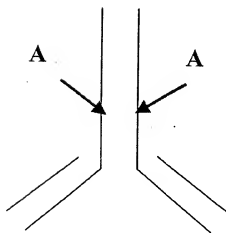
2. Galactosyltransferase, UDP-Gal

↓ 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D

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a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51A

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CHO, BHK, 293 cells, Vero expressed Remicade.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = PEG.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed Remicade.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.



1. galactosyltransferase,
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when a, c (independently selected) is 1;
R = PEG.

FIG. 51C

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Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

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CHO, BHK, 293 cells, Vero expressed Reopro.
a-m, r-u (independently selected) = 0 or 1;
n = 0; v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
n = 0; R = PEG; z = 1.

FIG. 52B

Insect cell expressed Reopro.
a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;
z = 1.



1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
e, g, i, r, t, v, x (independently selected) = 0 or 1;
v, x (independently selected) = 1,
when e, g (independently selected) is 1;
z = 1; R = PEG.

FIG. 52C

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Yeast expressed Reopro.

a-n = 0; r-y (independently selected) = 0 to 1;

z = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

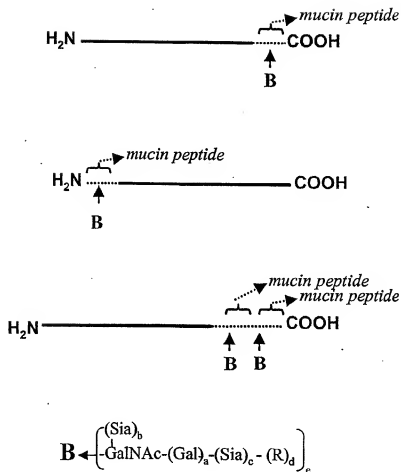
1. Endo-H

2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 52D

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a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 52E

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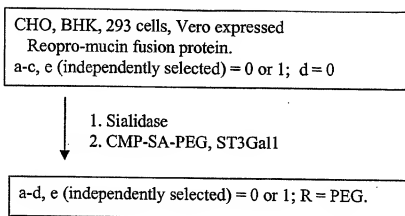


FIG. 52F

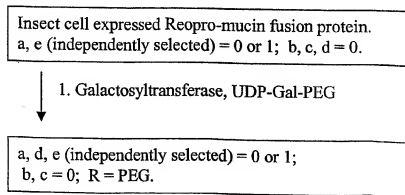


FIG. 52G

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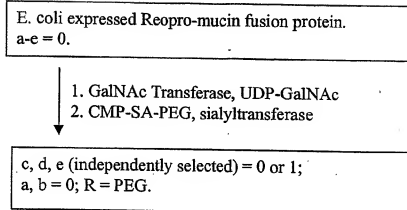


FIG. 52H

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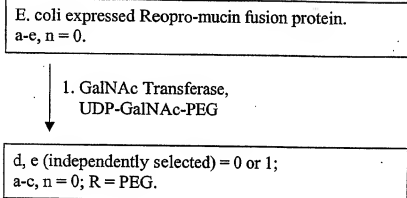


FIG. 52J

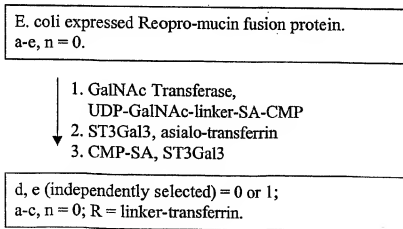


FIG. 52K

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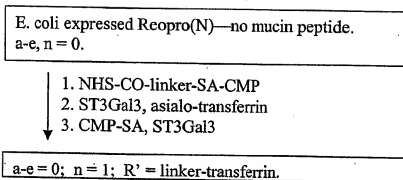
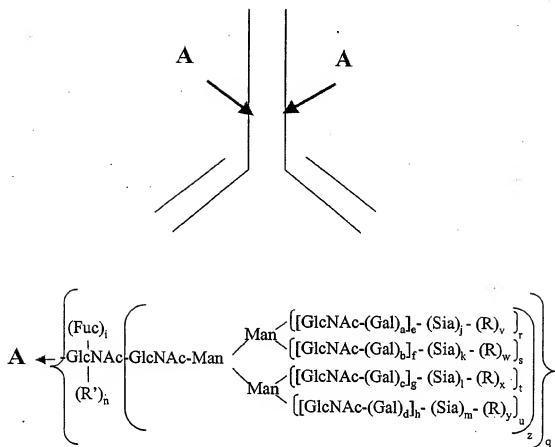


FIG. 52L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 53A

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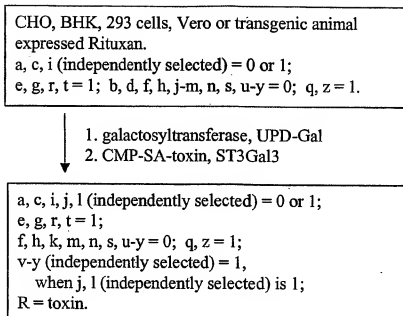


FIG. 53B

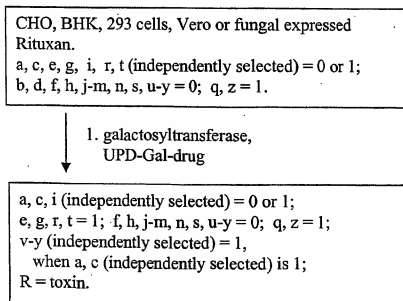


FIG. 53C

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Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

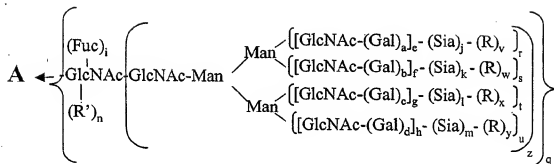
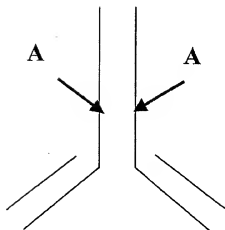
↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 53E

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CHO, BHK, 293 cells, Vero or transgenic animal
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
q, z = 1; v-y (independently selected) = 1,
when j, l (independently selected) is 1;
R = PEG.

FIG. 53F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;

R (independently selected) = mannose, oligomannose,
polymannose.

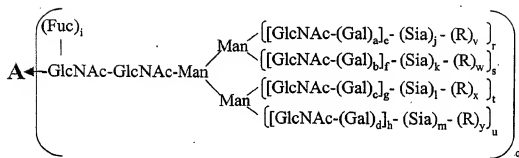
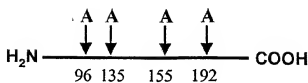


1. mannosidases (alpha and beta)
2. GNT-I,II, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;
R' = -Gal-radioisotope complex.

FIG. 53G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = mannose, polymer.

FIG. 54A

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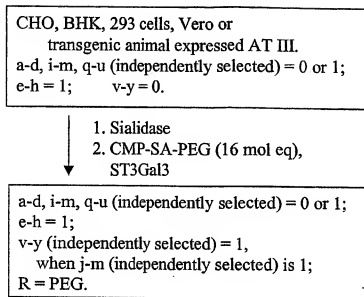


FIG. 54B

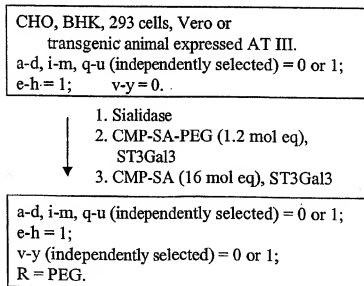


FIG. 54C

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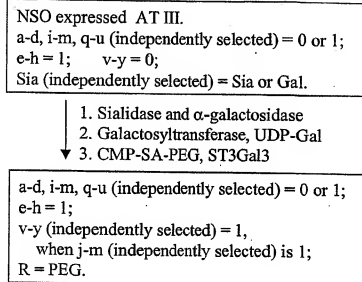


FIG. 54D

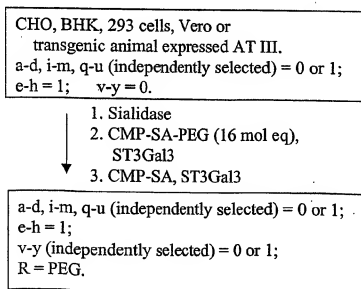


FIG. 54E

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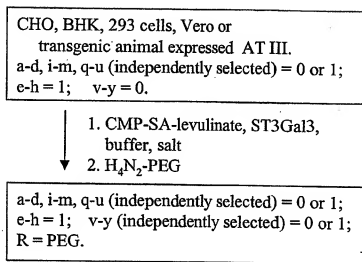


FIG. 54F

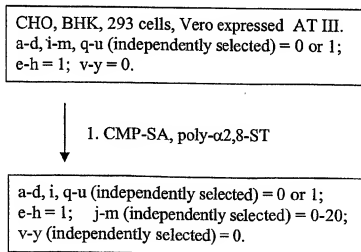
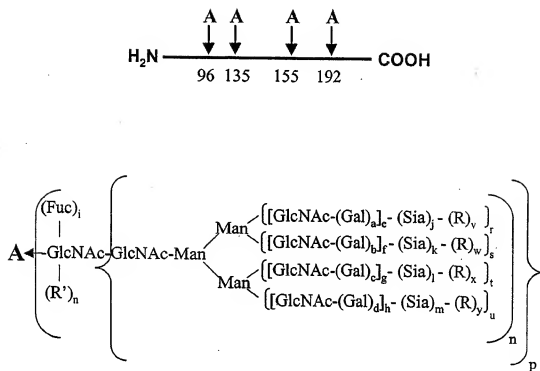


FIG. 54G

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

R' = H, sugar, glycoconjugate.

FIG. 54H

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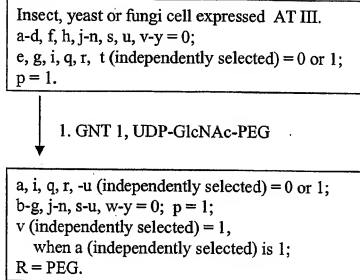


FIG. 54I

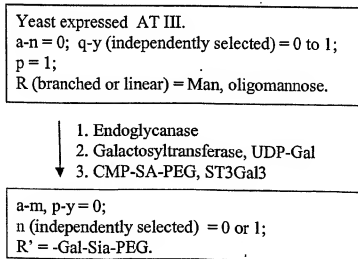


FIG. 54J

255/498

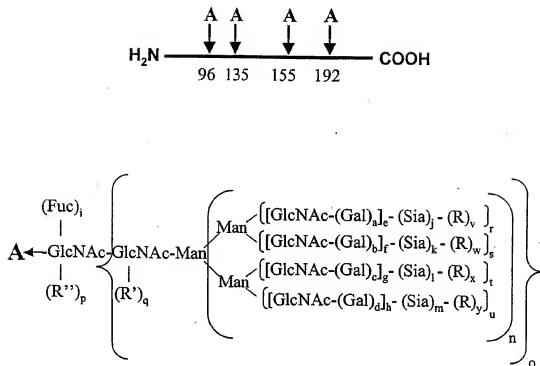
CHO, BHK, 293 cells, Vero expressed AT III.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 54K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

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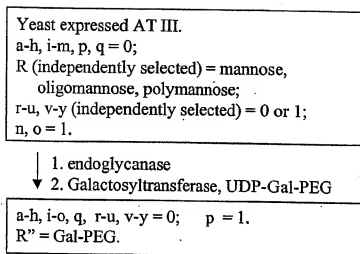


FIG. 54M

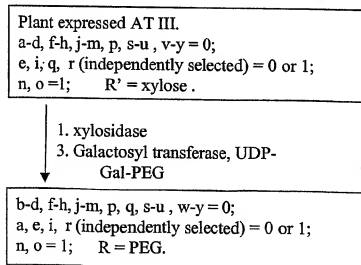


FIG. 54N

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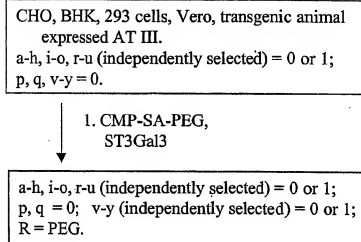
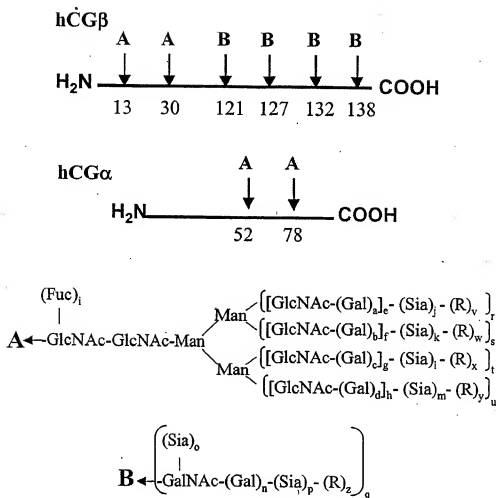


FIG. 54O

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer

FIG. 55A

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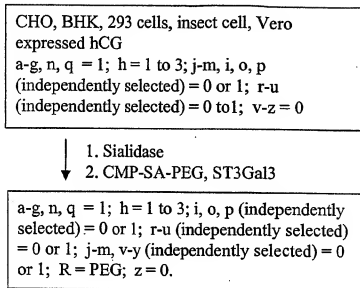


FIG. 55B

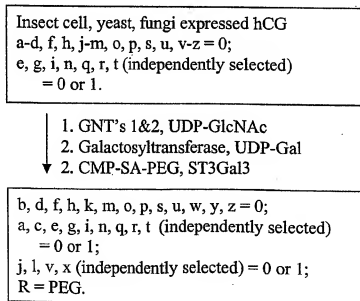


FIG. 55C

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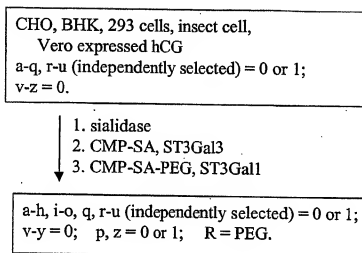


FIG. 55D

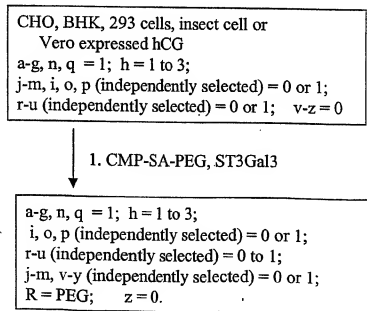


FIG. 55E

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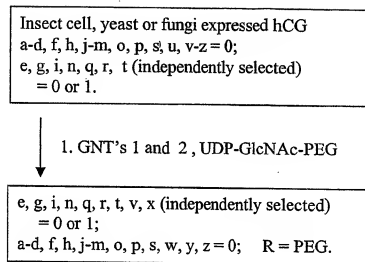


FIG. 55F

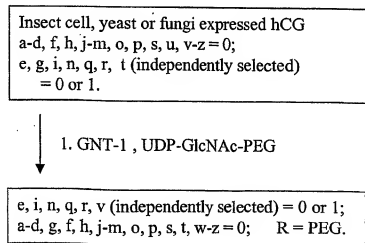


FIG. 55G

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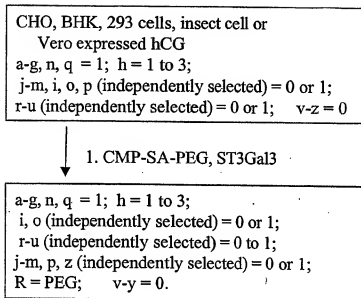


FIG. 55H

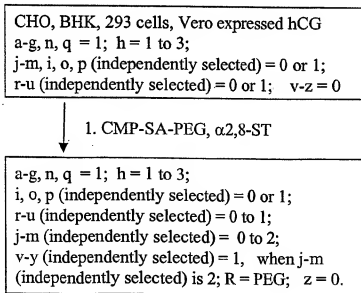


FIG. 55I

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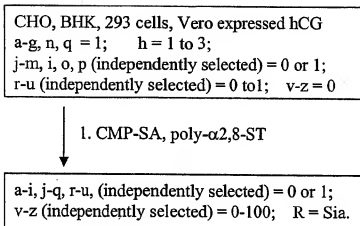


FIG. 55J

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CHO, BHK, 293 cells, insect cells, Vero expressed and secreted alpha-galactosidase
 a-h, i-m, q-u (independently selected) = 0 or 1;
 z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

- ↓
 1. Endo-H
 2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
 n, v-y = 0; z = 1; and when z = 0 and q = 1,
 then n (independently selected) = 0 or 1;
 R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,
 Vero expressed and secreted alpha-galactosidase
 a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

- ↓
 1. Sialidase
 2. CMP-SA-linker-Mannose-6-phosphate
 ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;
 n = 0; z = 1; R = mannose-6-phosphate; and when a-n = 0, then r-u (independently selected) = 0 or 1;
 v-y (independently selected) = 0-100;
 R = mannose or mannose with mannose-6-phosphate.

FIG. 56C

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NSO expressed alpha-galactosidase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;
v-y (independently selected) = 1, when j-m (independently selected) is 1; R = mannose-6 phosphate

FIG. 56D

CHO, BHK, 293 cells, Insect cells, Vero expressed and secreted alpha-galactosidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;

n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;

R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
 2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0; z = 1; R = PEG; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y = 0-100; R = mannose or mannose with mannose-6-phosphate.

FIG. 56E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,
fungi expressed alpha-galactosidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G

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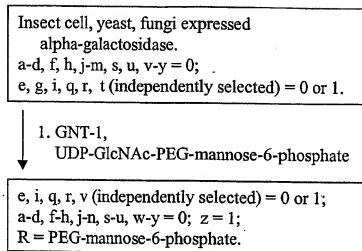


FIG. 56H

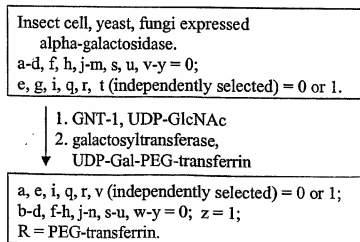


FIG. 56I

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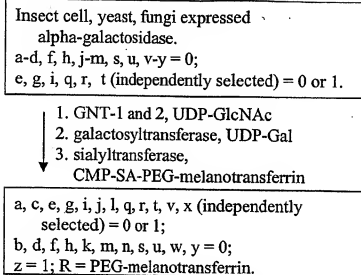
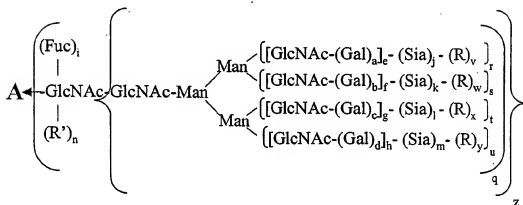
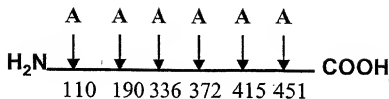


FIG. 56J

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a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

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CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Endo-H
↓
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
↓
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = mannose-6-phosphate; and when a-n = 0,
then r-u (independently selected) = 0 or 1;
v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

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NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;
v-y = 0; Sia (independently selected) = Sia or Gal.

1. Sialidase and α -galactosidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;
n, v-y = 0; and when a-n = 0, then r-u (independently
selected) = 0 or 1; v-y (independently selected) = 0-100;
R = mannose or mannose with mannose-6-phosphate.

1. Sialidase
2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;
z = 1; R = PEG; and when a-n = 0, then r-u
(independently selected) = 0 or 1; v-y = 0-100;
R = mannose or mannose with mannose-6-phosphate.

FIG. 57E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-iduronidase.
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;
r-u (independently selected) = 0 or 1; j-m (independently
selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate;
v-y (independently selected) = 0 or 1;
R = mannose-linker-ApoE.

FIG. 57F

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi
expressed alpha-iduronidase.
a-i, v-y = 0; q (independently selected) = 0 or 1;
z = 1; r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0-100;
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H
2. galactosyltransferase,
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;
R' = galactose-linker-alpha2-macroglobulin.

FIG. 57G

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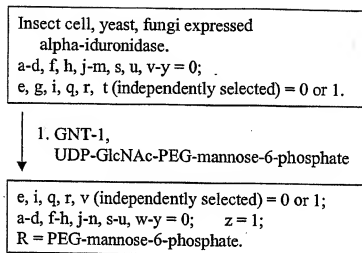


FIG. 57H

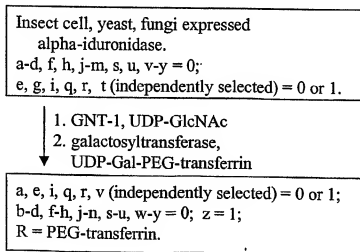


FIG. 57I

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Insect cell, yeast, fungi expressed
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

c, g, i, q, r, t (independently selected) = 0 or 1.

- ↓
1. GNT-1 and 2, UDP-GlcNAc
2. galactosyltransferase, UDP-Gal
3. sialyltransferase,
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J

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FIG. 58A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT
GCTGCTCGGACACTCTCTGGGCATCCCTGGGCTCCCTTGAGCAGCTG
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA
GCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT
CCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT
TTCCAGCGCCGGGCAGGAGGGGTCCTGGTTGCCTCCCATCTGCAGAG
CTTCTGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCCAGCCCTG
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
Leu Ala Gln Pro

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FIG. 59A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA
AGAAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAACATTAACTTTAT
ACTTTTAAATTATATAGAATAGAGATATACATAGGATATGTAAA
TAGATACACAGTGTATATGTGATTAAAAATAATAGGGAGATTCAATC
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA
AAGAGTGATAAAGAAAGCAAAAAGAGAAGTAGAAAAGTAACACAGG
GGCATTGTGGAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCTGGGTAGCAGG
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTTTTCTCC
TGCTTGAAGGACAGACATGACTTTGGATTTCCTCAGGAGGAGTTTGG
CAACCAGTTCAAAAGGCTGAAACCATCCCTGTCTCCATGAGATGA
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT
GGGATGAGACCCTCCTAGACAAAATTCTACACTGAACTCTACCAGCAG
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT
GCCTGGGAGGTTGTGAGAGCAGAAATCATGAGATCTTTTTCTTTGTCA
ACAAACTGTGAAGAAAGTTTAAGAAGTAAGGAATGAAAAGTGGTTCA
ACATGGAAATGATTTTCATTGATTCGTATGCCAGCTACCTTTTTATG
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACTATTGTATTCAG
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT
ATCTATTTAAATATTTTTAAAAATATTATTTATTTAACTATTTATAAAAC
AACTTATTTTGTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTTGTT
CATTGAACCTTTTGTATGGAACCTTTGTACTTGTATTCTCTTAAAAATG
AAATCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA
CTTCACTTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC
TAACAAATACAATTCTGCTCTCTCTGTGTATTTGATTTTGTATGAAAA
AAACTAAAAATGGTAATCATACTTAATTATCAGTTATGGTAAATGGT
ATGAAGAGAAGAAGGAACG

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FIG. 59B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser
 Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr
 Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
 Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
 Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu
 Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
 Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
 Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
 Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu
 Arg Ser Lys Glu

FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT
 AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCTA
 CTTAGCAGGAACACCTTGTTGCTTCTGCACCAAATGAGGAGAATCTCC
 CCTTTCTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCCCCAGGAG
 ATGGTAAAAGGGAGCCAGTTGCAGAAAGGCCCATGTTCATGTCTGTCT
 CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC
 CTCTGCTGCCTGGAACATGACCCTCCTAGACCAACTCCACACTGGACT
 TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTAGTGG
 GAGAAGGAGAAATCTGCTGGGGCAATTAGCAGCCCTGCACCTGACCTTG
 AGGAGGTACTTCCAGGGGAATCCGTGTCTACCTGAAAAGAGAAGAAATA
 CAGCGACTGTGCCTGGGAAGTTGTGTCAGAAATGAAAATCATGAAATCCT
 TGTTCCTTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA
 GACCTGGGCTCATCTTGA

FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val
 Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr
 Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp
 Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys
 Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His
 Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr
 Gly Leu His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
 Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe
 Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Val
 Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln Glu Arg
 Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser

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FIG. 60A

ATGACCAACAAGTGTCTCTCTCCAAATTGCTCTCCTGTTGTGCTTCTCC
 ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAGA
 AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG
 GCTTGAATATTGCCTCAAGGACAGGATGAACCTTGACATCCCTGAGG
 AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGATTGACC
 ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA
 TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA
 TGTCTATCATCAGATAAACCATCTGAAGACAGTCTTGAAGAAAAAC
 TGGAGAAAGAAGATTTTACCAGGGGAAAACATGAGCAGTCTGCAC
 CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA
 GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAATCCTAAGGA
 ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT
 CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTCAAGCATTCTTC
 AACCAGCAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCAAAAT
 GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT
 TTTATTTAT TTAATTTTATTTTGGAAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala
 Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp
 Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu
 Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp
 Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile
 Leu His Tyr Leu Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
 Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

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FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCTTGAGGAGCTGCGGG
CGGGCTCCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA
GAATGGGGGCTCCTGCAAGGACCAGTCCAGTCCATATATCTGCTTCT
GCCTCCCCTGCCTTCGAGGGCCGGAACCTGTGAGACGCACAAGGATGAC
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG
TGACCACACGGGCACCAAGCGCTCCTGTGCGGTGCCACGAGGGGTACT
CTCTGCTGGCAGACGGGGTGTCTGCACACCCACAGTTGAATATCCA
TGTGGAATAATACCTATTCTAGAAAAAAGAAATGCCAGCAAAACCCCA
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCAAAGGGGAGTGTCCA
TGGCAGGTCTCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACCAACACGACATC
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTGGTG
CCCCTCTGCCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC
GTGCTCTTCTCATTTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG
CGCCACGGCCCTGGAGCTCATGGTGTCTCAACGTGCCCGGCTGATGA
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT
ATCAGGAGTACATGTTCTGTGCCGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGGCCACATGCCACCCACTACCGGG
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA
ACCGTGGGGCACTTTGGGGGTACACCAGGGTCTCCAGTACATCGA
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCAGGAGTCTCTC
TGCAGCCCCATTTC

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FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

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FIG. 62A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT
GATCATGAAAAACGCCAACAAAAATCTGAATCGGCCAAAAGAGGTATAA
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT
GTATGGAAGAAAAGTGTAGTTTTGAAGAACCACGAGAAGTTTTTGAA
AACACTGAAAAGACAACCTGAATTTTGGAAGCAGTATGTTGATGGAGA
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGA
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT
GCCATTTCCATGTGGAAGAGTTTCTGTTTCAAAACTTCTAAGCTCAC
CCGTGCTGAGGCTGTTTTTCTGTATGTGGACTATGTAATCCTACTGA
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA
TTCCCTTGGCAGGTGTTTTTGAATGGTAAAGTTGATGCATTCTGTGGA
GGCTCTATCGTTAATGAAAAATGGATTGTAACCTGCTGCCACTGTGTT
GAAACTGGTGTAAAAATTACAGTTGTCGCAGGTGAACATAATATTGA
GGAGACAGAAACATACAGAGCAAAAAGCGAAATGTGATTGAGCAATT
ATTCTCCACCACACTACAATGCAGCTATTAATAAGTACAACCATGA
CATTGCCCTTCTGGAACCTGGACGAACCCCTAGTGTCAAAACAGCTACG
TTACACCTATTTCATTGCTGACAAGGAATACACGAACATCTTCTCA
AATTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTGAC
CGAGCCACATGCTTCGATCTACAAAAGTTACCATCTATAACAACAT
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAGGGACCAGTTTCTTA
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCCAAATA
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAAGGAAA
AAACAAAGCTCACITTAATGAAAGATGGATTTC AAGGTTAATTCATT
GGAATTGAAAATTAACAG

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FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

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FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCTG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCA
GAATGCACGCTACAGGAAAACCCATTCTTCTCCACGCCGGGTGCCCC
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCC
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTACCTCAG
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG
GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT
GTGAGATAAACTCTCCTTTTCCTTACCATACCACTTTGACACGCCTTC
AAGGATATACTGCAGCTTTACTGCCCTTCCTCCTTATCCTACAGTACAA
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAGCTTG
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

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FIG. 63C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG
ATTGTA CTGTGCGAGGCCTGGGGCCAGCTACTGCTCCTTTGGTGAAA
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

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FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT
GCACCGCCGAGCTTCCCCGGATGAGGGCCCCCGGTGTGGTCACCCGG
CGCGCCCCAGGTGCTGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG
GTGCACGAATGTCCTGCTGGCTGTGGCTTCTCCTGTCCCTGCTGTGCTG
CTCCTCTGGGCCCTCCAGTCTCTGGGCGCCCCACCACGCCTCATCTGT
GACAGCCGAGTCTCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAAGGAT
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG
CTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGCGAGCCAGAAGG
AAGCCATCTCCCCCTCAGATGCGGCCTCAGCTGCTCCACTCCGAACA
ATCACTGCTGACACTTTCGCAAACCTCTTCGAGTCTACTCCAATTC
CTCCGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC
TCACCAACATTGCTGTGTCCACACCCCTCCCCCGCCACTCCTGAACCCC
GTGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC
AACTCTGAGATCTAAGGATGTACAGGGCCAACTTGAGGGCCAGAG
CAGGAAGCATTAGAGAGCAGCTTTAAACTCAGGGACAGGCCATG
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC
AGGACACGCTTTGGAGGCGATTTACCTGTTTCGCACCTACCATCAGG
GACAGGATGACCTGGGAACTTAGGTGGCAAGCTGTGACTTCTCCAG
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCCTCTGG
CTCTCATGGGGTCCAAGTTTGTGTATTCTTCAACCTCATTGACAAGA
ACTGAAACCACCAAAAAAAAAAAAAA

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FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu Leu Ser
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

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FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT
CTCTGCACCCGCCCCGCTCGCCAGCCCCAGCACGCAGCCCTGGGAGC
ATGTGAATGCCATCCAGGAGGCCGCGTCTCCTGAACCTGAGTAGA
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAAT
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA
ACCTGAAGGACTTTCTGCTTGTATCCCCTTTGACTGCTGGGAGCCAG
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

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FIG. 67A

ATGAAATATACAAGTTATATCTTGCTTTTCAGCTCTGCATCGTTTGG
GGTTCTCTTGCTGTTACTGCCAGGACCCATATGTAAAAAGAAGCAGA
AAACCTTAAGAAATATTTTAATGCAGGTCATTTCAGATGTAGCGGATA
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACT
TTTTAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT
GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG
AACTGTGCGCCAGCAGCTAAAAACAGGGAAGCGAAAAAGGAGTCAGAT
GCTGTTTCGAGGTGCAAGAGCATCCCAAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
Leu Lys Asn Trp Lys Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

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FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC
CAGGAACCTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAAGCCTTC
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG
ATTACGTGGAGAAGGGTACTCAAGGGAATTTGTGGATTTGGTCAAG
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTTT
AAAGGCAAAATGGGAGAGACCCCTTTGAAGTCAAGGACACCGAGGAAG
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG
AAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAG
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAATGAAGTCAAC
CACGATATCATCACCAAGTTTCTGGAAAATGAAGACAGAAGGTCTGC
CAGCTTACATTACCCAACTGTCCATTACTGGAACCTATGATCTGAA
GAGCGTCTGGGTCAACTGGGCATCACTAAGGTCTTTCAGCAATGGGG
CTGACCTCTCCGGGGTACAGAGGAGGCACCCCTGAAGCTCTCCAAG
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAAGGACTGAAGC
TGCTGGGGCCATGTTTTAGAGGCCATACCCATGTCTATCCCCCGGA
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAAATAC
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT
AACTGCCTCTCGTCTCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC
CTGGATGACATTAAAGAAGGGTTGAGCTGG

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FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val
Phe Ala LeuVal Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
Phe Leu Glu Asn Glu AspArg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val
Val Asn Pro Thr Gln Lys

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FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTT
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGGGTCT
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTC AAGTCCTTCCA
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCTGGGCATCAGGT
GCCCCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCGACCTTTCCT
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG
GCCTGCTACTGACCCTGCAGCCAGAACAGAAGTCCAGAAAAGTGAAG
GGATTGGAGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC
CTGTACACCCCTGCCCAAAATTTGCTACTTAAATCGTACTTCTCTGAA
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA
GTTGCACAACCTCAGCCTCCCAGAGGAAGATACCAAGCTCAAGATAC
CCCTGATTACCCAGCCCTGCAGTTGGCCAGCGTCCGTTTCACTCC
TTGCCAGCCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG
GTGAATGGGAAGGGGTCACTCAAGGACAGCCCGGAGACATCTACC
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG
AGCACAAGTATACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTACCCCT
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCTACCCCTCGCC
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACTGGACTTTCT
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA
ACACCATGCTCTTTGCCTCAGAGGCCCTGTGTGGGCTCCAAGTTCTGGG
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC
CACAGCATCATCAGAACCTCCTGTACCATGTGTGCGGTGGACCGAG
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA
CTTGTGCGACAGTCCCATCATTGTAGACATCACC AAGGACAGGTTTAA
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC
TGAGGGCTCCCAAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC
TGGACGCAGTGGCAGTGTGATGCATCCCGATGGCTGTCTGTTGTGGTCTG
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG
CTGTGGGCTTCTCGAGACAATCTCACCTGGCTACTCCATTCAACCT
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCAGTGG
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG
TGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

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FIG. 69A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCTCTAGGTGGT
 GCCCAGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTG
 CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT
 TGGAAACT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser
 Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser
 Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys
 Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr
 Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu-Ser Met Gly
 Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 Lys Phe Gln Lys Val Lys Gly Phe Gly Ala Met Thr Asp Ala Ala Ala Leu
 Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser
 Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
 Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser
 Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu
 Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
 Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile
 Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu
 His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
 Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp
 Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg
 Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val
 Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro
 Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
 Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu
 Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr
 Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu
 Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn
 Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
 Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

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FIG. 70A

ATGGATGCAATGAAGAGAGGGGCTCTGCTGTGTGCTGCTGTGTGG
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCCGATTACAGAA
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAACGCA
GATGATATACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA
GCAACCGGGTGGAAATATTGCTGGTGCAACAGTGGCAGGGCAGAGTGC
CACTCAGTGCCTGTCAAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG
GGGCACCTGCCAGCAGGGCCCTGTACTTCTCAGATTTCGTGTGCCAGTG
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCA
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGGCACGTGGAGCAC
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG
GCCTGGGGAACCAACTACTGCAGAAACCCAGATCGAGACTCAAA
GCCCTGGTGCTACGTCTTTAAGCGGGGAAGTACAGCTCAGAGTTCT
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC
CTCCTGCCTCCCGTGGAAATTCATGATCCTGATAGGCAAGGTTTACAC
AGCACAGAACCCCAAGTGGCCAGGCACTGGGCCCTGGGC AAAACATAATT
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG
GAGGGCTCTTTCGCCGACATCGCCTCCCAACCCCTGGCAGGCTGCCATCT
TTGCCAAGCAGCAGGAGGTGCGCCGGGAGAGCGGTTCTGTGCGGGGGC
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG
GAGAGGTTTCCGCCCCACCACTGACGGTGATCTTGGGCAGAACATA
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
TACATTGTCCATAAGGAATTTCGATGACACTTACGACAATGACAT
TGCGCTGCTGCAGCTGAAATCGGATTTCGTCCCGCTGTGCCCAGGAGA
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG
CCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC
CTTGCTCTCTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTACAGCT
GTACCCATCCAGCCGCTGCACATCACAAACATTTACTTAACAGAACAG
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGGCGGGCCC
CAGGCAAACTTGACGACGCCTGCCAGGGCGATTCCGGGAGGCCCCCT
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGTGTGTACACCAAG
GTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGACC
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

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FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Gln Lys Phe Glu Val Glu Lys
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg
Asp Asn Met Arg Pro

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FIG. 71A

ATCACTCTCTTAACTCACTACTCACATTAACCTCAACTCCTGCCACAA
TGTACAGGATGCAACTCCTGTCTTGCAATTGCACTAATTCTTGCACTTG
TCACAAACAGTGCACCTACTTCAAGTTCGACAAAAGAAAACAAAAGAAA
ACACAGCTACAACCTGGAGCATTACTGCTGGATTTACAGATGATTTTG
AATGGAATTAATAATTACAAGAATCCCCAAACTCACCAGGATGCTCAC
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC
AGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTGCTGAATTTA
GCTCAAAGCAAAAACCTTCACTTAAGACCCAGGGACTTAATCAGCAA
TATCAACGTAATAGTTCTGGAACATAAGGGATCTGAAACAACATTCA
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAAGTTGATAA
TTAAGTGCTTCCCACTTAAACATATCAGGCCTTCTATTTATTTATTTA
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG
TAACTATTATTCTTAATCTTAAAACTATAAATATGGATCTTTTATGAT
TCTTTTTGTAAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC
CAAAAATATTTATTTATTTATGTTGAATGTTAAATATAGTATCTATGTAG
ATTGGTTAGTAAAACTATTTAATAAAATTTGATAAATATAAAAAAAAAA
AAACAAAAAAAAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
Gln Ser Ile Ile Ser Thr Leu Thr

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FIG. 72A-1

ATGCAAAATAGAGCTCTCCACCTGCTCTTTCTGTGCTTTTGCATTCT
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTCA
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG
ATTTCTCCTAGAGTGC AAAATCTTTCCATTCAACACCTCAGTCGT
GTCAAAAAGACTCTGTTGTAGAAATTCACGGATCACCTTTTCAACAT
CGCTAAGCCAAAGGCCACCTGGATGGGTCTGCTAGGCTCTACCATCC
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT
TCCCATCCTGTGAGTCTTCATGCTGTTGGTGTATCCTACTGGAAGCT
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG
AAGATGATAAAAGTCTTCCTGGTGAAGCCATACATATGTCTGGCAG
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG
CCTCATTTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG
AAAAGACACAGACCTTGCACAAAATTTATACTACTTTTGTCTGTATTTG
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATCA
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCTGAA
GTGCACTCAATATTCTCGAAGGTACACATTTCTGTGAGGAACCAT
CGCCAGGCGTCTTGGAAAATCTCGCCAATAACTTTCTTACTGCTCAA
ACACTCTTGATGGACCTTGGACAGTTCTACTGTTTGTGCATATCTCTT
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT
CCAGGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG
ACTATGATGATGATCTTACTGATTCTGAAATGGATGCTGGTCAAGTTTG
ATGATGACAACCTCTCCTTCTTATCCAAATTCGCTCAGTTGCCAAGA
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC
TGGGACTATGCTCCCTTAGTCTCGCCCCGATGACAGAAGTTATAAA
AGTCAATATTTGAACAAATGGCCCTCAGCGGATTGGTAGGAAGTACAA
AAAAGTCCGATTTATGGCATACACAGATGAAACCTTTAAGACTCGTG
AAGCTATTTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG
AAGTTGGAGACACACTGTTGATTATTTAAGAATCAAGCAAGCAGA
CCATATAACATCTACCCTCACGGAATCACTGATTCGCTCTTTGTAT
TCAAGGAGATTACCAAAAGGTGTAAAAACATTTGAAGGATTTTCCAAT
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGAAGTGTAGAAG
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC
TCCTCATCTGTACAAAAGAATCTGTAGATCAAAGAGGAAACCGATA
ATGTCAGACAAGAGGAATGTCATCCTGTTTCTGTATTTGATGAGAAC
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTCTCCCCAATCCA
GCTGGAGTGCAGTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT
GCACAGATCAAGTGGCTATGTTTTGATAGTTTGAGTTGTCAAGTTTG
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTTGGAGACAGAG
CTGACTTCCTTTCTGTCTCTTCTCTGGATATACCTTCAAACACAAAAT

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FIG. 72A-2

GGTCTATGAAGACACACTCACCTATTCCCATTCTCAGGAGAAACTGT
CTTCATGTGCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA
ACTCAGACTTTCCGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT
AGTTGTGACAAGAACACTGGTGATTATTACGAGGACAGTTATGAAGA
TATTTTCAGCATACTTGTCTGAGTAAAAACAATGCCATTGAACCAAGAA
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAGCAATTT
AATGCCACCACAATTCCAGAAAAATGACATAGAGAAGACTGACCCCTG
GTTTGACACAGAACACCTATGCCTAAAAATACAAAATGTCTCCTCTA
GTGATTGTGTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT
CCTTATCTGTATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA
CACTTCAGGCCACAGCTCCATCAGTGGGGACATGGTATTTACCCC
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGACAACTG
CAGCAACAGAGTTGAAGAAACTTGATTTCAAAGTTTCTAGTACATCA
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT
GATAATACAAGTTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT
AGTCAATTAGATACCACTCTATTGTGGCAAAAAGTCATCTCCCCCTACT
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAAATGATTCAAA
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA
AAAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGAAAAAGA
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAAGTT
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT
AATAGAAAGACTCAGCATTGATGGCCCATCTATTATAATTGAGATAG
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA
AAGTGACACCTTTGATTTCATGACAGAATGCTTATGGACAAAAATGCT
ACAGCTTTGAGGCTAAATCATATGTCAAATAAAACTACTTCATCAAAA
AAACATGGAAATGGTCCAACAGAAAAAGAGGGCCCCATCCACCA
GATGCACAAAATCCAGATATGTCGTTCTTTAAGATGCTATTCTTGCCA
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG
AAAAATCTGTGGAAGGTCAGAATTTCTGTCTGAGAAAAACAAAGTG
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA
TGTTTTTCCAAGCAGCAGAAACCTATTCTTACTAAGTTGGATAATT
TACATGAAAAATAATACACACAATCAAGAAAAAATAATTCAGGAAGA
AATAGAAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC
AGATACATACAGTGACTGGCAGTAAAGAAATTCATGAAGAACCTTTTC
TTACTGAGCACTAGGCAAAATGTAGAAGGTTTCATATGACGGGGCATA
TGCTCCAGTACTTCAAGATTTTAGGTCATTAATGATTCAACAAATAG
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA
AAGTTGGAAGGCTGGGAAATCAAACAGCAAATGTAGAGAAATAT
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAAATTTG
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCACTA

FIG. 72A-3

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GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCCCTCACAC
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAATAGTA
TCTCCATTACCCATTGCAAAAGGTATCATTTCCATCTATTAGACCTA
TATATCTGACCAGGGTCTATTCCAAGACAACCTTCTCATCTTCCAG
CAGCATCTTATAGAAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT
TTCTTACAAGGAGCCAAAAAAATAACCTTTCTTTAGCCATTCTAACC
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG
TGCCACAAATTTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC
GAAACCAGACTTGCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA
AAGTTCACATTTATCAGAAGGACCTATTCCTACGGAAACTAGCAATG
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA
CAGAGGGAGCGATTAAGTGAATGAAGCAAACAGCCTGGAAAAAGT
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAGAGACTCCCTCAA
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC
AAAAGAAGAGTGGAAAATCCCAAGAGAAAGTCACCAGAAAAAACAGCT
TTTAAGAAAAAGGATACCATTGTTGCCCTGAACGCTTGTGAAAAGCAAT
CATGCAATAGCAGCAATAAAATGAGGGACAAAAATAAGCCGAAATAG
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA
AACCCACCAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAAAT
AGAGCCCCCGCAGCTTTCAAAAAGAAACACGACACTATTTTATTGCTG
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAGAAAGT
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT
GGAGAATCAAAATGAACATTTGGGACTCTGGGGCCATATATAAGAGC
AGAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC
GTCCCTATTCTTCTATTCTAGCCTTATTCTTATGAGGAAGATCAGAG
GCAAGGAGCAGAACCTAGAAAAAATTTGTCAAGCCTAATGAAACCA
AACTCTATTTTGGAAAAGTGCAACATCATATGGCAACCCACTAAAGAT
GAGTTTGACTGCAAAGCCTGGGCTTATTCTCTGATGTTGACCTGGAA
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT
TGCTCTGTTTTTACCATCTTTGATGAGACCAAGCTGGTACTTCACT
GAAAAATATGGAAGAAAGTGCAGGGCTCCCTGCAATATCCAGATGGA
AGATCCCACTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAAACATCCATTCT
ATTCAATTCAGTTGGACATGTGTTCACTGTACGAAAAAAGAGGAGTA
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGGAGACAGTGA

FIG. 72A-4

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AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGGAATGCCTTATTGG
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA
TAAGTGTGAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG
CCAGACTTCATTATTCCGGATCAATCAATGCTGGAGACCAAGGAG
CCCTTTTTCTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTAC
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA
CTTATCGAGGAAATCCACTGGAACCTTAATGGTCTTCTTTGGCAATG
TGGATTCATCTGGGATAAAAAACAATATTTTTAACCCCTCCAATTATTG
CTCGATACATCCGTTTGACCCAACTCATTATAGCATTTCGAGCACTC
TTCGCATGGAGTTGATGGGCTGTGATTAAATAGTTGCAGCATGCCAT
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA
TCCACTTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA
CAGGAGTAACTACTCAGGGAGTAAAATCTCTGCTTACCAGCATGTAT
GTGAAGGAGTTCCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC
TCTCTTTTTTTCAGAAATGGCAAAGTAAAGGTTTTTCAGGGAATCAAGA
CTCCTTCACACCTGTGGTGAACCTCTCTAGACCCACCCTTACTGACTCG
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC
CACTGCAGCACCTGCCACTGCCGTCACCTCTCCCTCCTCAGTCCAGG
GCAGTGTCCCTCCCTGGCTTGCCCTTCTACCTTTGTGCTAAATCCTAGC
AGACACTGCCTTGAAAGCCTCCTGAATTAACATATCATCAGTCTGCATT
TCTTTGGTGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTCTTA
CCTATTTTCTGCAGCTGCTCCAGATTACTCTTCTTCCAATATAACT
AGGCAAAAAGAAGTGAGGAGAAAACCTGCATGAAAGCATTCTTCCCTG
AAAAGTTAGGCCTCTCAGAGTCACCACTTCTCTGTGTAGAAAACT
ATGTGATGAACTTTGAAAAAGATATTTATGATGTTAACATTTCAGGT
TAAGCCTCATACGTTTAAAAATAAACTCTCAGTTGTTTATTATCCTGA
TCAAGCATGGAACAAGCATGTTTCAGGATCAGATCAATACAATCTT
GGAGTCAAAAGGCCAAATCATTTGGACAATCTGCAAAATGGAGAGAA
TACAATAACTACTACAGTAAAGTCTGTTTCTGCTTCTTACACATAGA
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA
AACTGACTTCTTAAACTGAGAATTATAGATGGGGTCAAGAATCCC
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAATGTGC
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT
GACCAATAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA
AAATGATGA

FIG. 72B-1

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Leu Gly Ala Glu Tyr
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
His Lys Met Val Tyr Glu Asp Thr Leu Phe Pro Phe Ser Gly Glu Thr Val
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

FIG. 72B-2

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Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
 Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn
 Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln
 Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp
 Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu
 Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu
 Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
 Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
 Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr
 Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu
 Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu
 Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly
 Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn
 Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly
 Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly
 Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu
 Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp
 Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser
 Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
 Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser
 Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala
 Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg
 Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro
 Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu
 Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly
 Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp
 Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile
 Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
 Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln
 Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg
 Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys
 Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val
 Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe
 Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu
 Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn
 Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu
 Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile
 Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile
 Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

FIG. 72B-3 304/498

Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu
 Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
 Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr
 Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser
 Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro
 Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu
 Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys
 Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu
 Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu
 Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile
 Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
 Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu
 Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
 Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
 Tyr Gly Met Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
 Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro
 Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro
 Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
 Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu
 Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
 Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr
 Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
 Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
 Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr
 Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu
 His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr
 Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
 Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
 Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
 Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
 Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

FIG. 72B-4

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Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr

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FIG. 73A

TCCACCTGTCCCCGAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC
AATGAACTTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC
CCAAAGAAATTCGGAGGGCAGCACTGTGAAATAGATAAGTCAAAAAC
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG
ACACCATGGGCGGGCCCTGCCTGCCCTGGAACCTCTGCCACTGTCTTTC
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGCCCTGG
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCCTGG
TGCTATGTGCAAGTGGGCCTAAAGCCGCTTGTTCCAAGAGTGATGGT
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT
TAAAATTTCAGTGTGGCCAAAAGACTCTGAGGCCCGCTTTAAGATTA
TTGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTGCGGCC
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT
TGATTACCAAAGAAGGAGGACTACATCGTCTACCTGGGTGCTCAA
GGCTTAACCTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGA AAAAC
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA
AGCTGATTTCCCACCGGAGTGTGTCAGCAGCCCCACTACTACGGCTCTG
AAGTACCAACCAAAAATGCTGTGTGCTGACCCACAGTCAGTGAAACGA
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA
GGGTCCCAAGGGAGGAAACGGGCACCAACCGCTTTCTTGCTGGTTGTC
ATTTTTGCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA
AGAT

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FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

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FIG.74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAAATTGTCATCA
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGCGCTGCTG
GCACTGGCGGCCCTACTGCAGGGGGCCGTGTCCCTGAAGATCGCAGC
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTTCGTGTA
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT
GTCAGGTTCTTCTCCCGTTTACAGAGGTCAGGGAGTTTGCCATTGTT
CCCCTGCATGCGGCCCGGGGACGCAGTAGCCGAGATCGACGCTCT
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTC
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG
CTGAAGTGAGCAGCCCCCTCCCCACACCAGTTGAACTGCAG

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FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
Glu Val Met Leu Lys

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FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG
CCCTGTGGATGCGCCTCCTGCCCTGCTGGCGCTGCTGGCCCTCTGGG
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA
GGTGGAGCTGGGCGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG
CAGCCCGCAGGCAGCCCCCACC GCCCCTCCTGCACCGAGAGAGA
TGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly
Pro Asp Pro Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

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FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT
TTCTGTTCCCAATCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCT
GCGTTCCGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC
GGGCCAGGGTTCACCCACCACACGGCGGTCTTTGGGGTGGAGCCC
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCTG
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAATCCACAACA
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGCCTATATTTTCCT
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCTGTTCCGACTACTGTC
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC
ATGGAGAGCACAACATCAGGATTCTAGGACCCTGCTCGTGTACA
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGAGCACCCACGTG
TCCTGGCCAAAATTGCGAGTCCCCAACCTCCAATCACTACCAACCTC
TTGTCTCCAATTTGTCTGGTTATCGCTGGATGTGTCTCGCGCGTTTT
ATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTGGTTC
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT
CAAGGAACCTCTATGTTTCCCTCTTGTGCTGTACAAAACCTTCGGAC
GGAAACTGCACCTGTATTCCCATCCCATCATCCTGGGCTTTCGCAAGA
TTCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA
GTGCCATTTGTGTCAGTGGTTCGACGGGCTTCCCCCACTGTTTGGCTTT
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT
TGAGTCCCTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC
ATTTGA

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FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
Trp Val Tyr Ile

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FIG. 77A

CGAACCCTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA
 CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC
 CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGC
 CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT
 TTGACACCTACCAAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG
 AAGTATTTCATTCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG
 TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA
 CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA
 GCCCCTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG
 CGCCTCTGACAGCAACGCTCTATGACCTCCTAAAGGACCTAGAGGAAG
 GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCGGACT
 GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA
 CAACGATGACGCTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG
 GAAGGACATGGCAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCG
 CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG
 TGACCCCTCCCAAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT
 GCCCACCAGCCTGTCTTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
 Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp
 Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
 Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
 Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
 Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
 Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
 Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
 Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
 Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

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FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT
TTATCTTTTGTCTTGTCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC
CATGAATCCCATGTGCATTTACCGCTCCCCGGAGAAGAAGGCAACTG
AGGATGAGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGGCG
TGCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGCTACCACTTTCTA
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCCTGTCT
ACCCCTGAGTATCTCCACGGCTTTTGTCTATGACCAAGCTGGGTGCTG
TAATGACACCCTCCAGCAACTGATGGAGGTATTTAAGTTTGACACCATT
ATCTGAGAAAAACATCTGATCAGATCCACTTCTTCTTTGCCAAACTGAA
CTGCCGACTCTATCGAAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC
CAATCGCCTTTTTGGAGACAAATCCCTTACCTTCAATGAGACCTACCA
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCTGGACT
TCAAGGAAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGTG
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTACTTCAA
GGGCTGTGGAAGTCAAAGTTCAGCCCTGAGAACACAAGGAAGGAAC
TGTTCTACAAGGCTGATGGAGAGTCTGTTTCAGCATCTATGATGTACC
AGGAAGGCAAGTTCGGTTATCGGCGCGTGGCTGAAGGCACCCAGGTG
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCTCATCTTG
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACCTCACCCC
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG
TGGTCCACATGCCCGCTTCCGCATTGAGGACGGCTTCAGTTTGAAGG
AGCAGCTGCAAGACATGGGCCCTGTGATCTGTTTCAGCCCTGAAAAA
TCCAAACTCCCAAGGTATTGTTGTCAGAAGGCCGAGATGACCTCTATGTC
TCAGATGCATTCCATAAGGCATTTCTTGAGGTAAATGAAGAAGGCAG
TGAAGCAGCTGCAAGTACCGCTGTTGTGATGCTGGCCGTTGCTATAA
CCCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCCTGGTTTTAT
AAGAGAAAGTTCCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA
ACCTTGTGTTAAGTAA

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FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
Trp Leu Asp Glu Leu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

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FIG. 79A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCAG
AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCA
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCCA
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA
GTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATGGG
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

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FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCA
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG
TGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGCG
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC
TCTGCCGCCGAGCACCCTGACTGCGGGGGTCCCAAGGACCACCCC
TTGACCTGTGATGACCCCGCTTCCAGGACTCCTCTCCTCAAAGGCC
CCTCCCCCAGCCTTCCAAGCCCATCCCGACTCCCGGGGCCCTCGGAC
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

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FIG. 80A

ATGCGTCCCCTGCGCCCCCGCGCCGCGCTGCTGGCGCTCCTGGCCTCG
CTCCTGGCCGCGCCCCCGGTGGCCCCGCGCGAGGCCCGCACCTGGT
GCAGGTGGACGCGGCCCGCGCGCTGTGGCCCCTGCGGCGCTTCTGGA
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCAGGCTGACCAG
TACGTCCTCAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA
GCTTGTCACCAACAGGGGGTCCACTGGACGGGGCCTGAGCTACAACT
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC
TCCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT
TTGAGGACAAGCAGCAGGTGTTTGAGTGGAAGGACTTGGTCTCCAGC
CTGGCCAGGAGATACATCGGTAGGTACGGA CTGGCGCATGTTTCAA
GTGGAACCTTCGAGACGTGGAATGAGCCAGACCACCACTTTGACA
ACGTCTCCATGACCATGCAAGGCTTCTGAACTACTACGATGCCTGCT
CGGAGGGTCTGCGCGCCGCCAGCCCCGCTGCGGCTGGGAGGCCCC
GGCGACTCCTTCCACACCCACCGCGATCCCCGCTGAGCTGGGGCCTC
CTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGAGGGCGGG
CGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCT
CCATCTCCATCCTGGAGCAGGAGAAGGTGCTGCGCAGAGTGCCGG
CAGCTCTTCCCCAAGTTCGCGGACACCCCCATTTACAACGACGAGGCG
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT
GACCTACGCGGCCATGGTGGTGAAGGTCACTCGCGCAGCATCAGAACC
TGCTACTGGCCAAACCAACCTCCGCTTCCCCTGCTGCTCCTGAGCA
ACGACAATGCCTTCTGAGCTACCACCCGACCCCTTCGCGCAGCGCA
CGCTCACCGCGCGCTTCCAGGTCAACAACACCCGCCCGCCGACGTG
CAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGGGCTGCTGCGCCT
GCTGGATGAGGACGAGCTCTGGGCCGAAGTGTCGACGGCCGGGACCG
TCCTGGACAGCAACCACACGGTGGGCGTCTGGCCAGCGCCACCGC
CCCCAGGGCCCGGCCGACGCTGGCGCGCCGCGGTGCTGATCTACGC
GAGCGACGACACCCGCGCCACCCCAACCGCAGCGTTCGCGGTGACCC
TGCGGCTGCGCGGGTGCCCCCGGGCCGGGCTGGTCTACGTCACG
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGCGCGG
CCTGGGCGCGCCGCTTCTCCCCACGGCAGAGCAGTTCGGCGCATGC
GCGCGGCTGAGGACCCGGTGGCCGCGGGCGCCCGCCCTTACCCGCC
GGCGGCCGCTGACCTGCGCCCCGCGCTGCGGCTGCCGTGCTTTTG
CTGGTCAAGTGTGTGCGCGCCCGAGAAGCCGGGAGGTAC
GCGGCTCCGCGCCCTGCCCTGACCAAGGGCAGCTGGTTCTGGTCTG
GTCGGATGAACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCC
AGTTCTCTCAGGACGGTAAGGCGTACACCCGGTCAGCAGGAAGCCA
TCGACCTTCAACCTCTTTGTGTTTACGCCAGACACAGGTGCTGTCTCT
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCGACCAAGCC
CTTCTCGGACCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC
CCCATCCCCGGGCAATCCAT GA

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FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu
Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala
Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu
Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala
Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu
Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His
Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu
Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val
Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly
Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp
Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys
Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
Phe His Thr Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp
Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His
Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln
Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala
Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala
Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr
Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro
His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu
Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala
Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro
Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu
Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp
Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg
Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu
Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala
Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln
Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr
Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro
Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr
Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro
Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

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FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCCT
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACT
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCTGC
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG
GATGGCTCCCCAAAGAGATTGAGAAGGCAGACTTCAGGCAGACCCTC
AGCGCTTCCTCATGGGATTGCCAGCTAGCTAATTATGTTACAGCA
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC
GCAGGCTTCCCTGGGAGTTTGGATACTACGACATTGATGCCAGACC
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGT
GACAGTTTGAAAAATTTGGCAGATGGTTATAAGCACATGTCCTTGGCC
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCTCTT
TATATGTGGCCCTTTCAAAAGCCCAATTATACAGAAATCCGACAGTAC
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAAGT
ATAAAGAGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTT
GATGTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGAT
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG
GAGACAACCTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG
GCTGTAGCTATGATAAAACCGCAGGAGATTGGTGGACCTCGCTCTTAT
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC
TGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTCTAT
GAATGGACTTCAAGGTTAAGAAGTCACATAAATCCACAGGCACTGT
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAGACTTACT
TTAA

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FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

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FIG. 82A

ATGGCGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCGCCAGGTGGCATTACACCCTA
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG
GACAGCACATACCCCAGCTCTGGAACCTGGGTCCCCGAGTGCTTGAG
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAACCTGAAACATCAGA
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC
ATCCACGGATATTTCAGAGCCCCACCAGATCTGTAACGTGGTGGCCAT
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCACGCCAGTGTC
ACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGCTCC
AAGCACCTCCTTCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAACGTGTGCATCATGAC
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCACTCGGAACACAGC
CACAGGCCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCGGGC
CAGCACCGGGAGCTCAGATTCTTCCCTGGTGGCCATGGGACCCAGG
TCAATGTACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT
CACAGTGTCTCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC
AGCCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCTTCTCCAAGGA
GGAATGTGCCTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGG
GGAGCACCGAAGAGAAGCCCCCTGCCCTTGGAGTGCCTGATGCTGGG
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTCTGATGCCAAGG
TGGGCTGAGCCCTGGCAGGATGACCTGCGAAGGGGCCCTGGTCTT
CCAGGC

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FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Leu Asp Arg
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
Asp Ala Gly Met Lys Pro Ser

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FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
Gly Thr Leu Val Thr Val Ser Ser

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FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 85A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA
 GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTTCGTTGGCTCAAGC
 ATCCACTGGTATCAGCAAAGAACAATGGTTCTCCAAGGCTTCTCATA
 AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC
 AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
 GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC
 ACGTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA
 GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT
 CCTGTGTTGCCTCTGGATTCAATTTTCAGTAACCACTGGATGAACTGGG
 TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA
 TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
 AGGTTACCATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA
 ATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG
 AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC
 ACAGTCTCC

FIG. 85B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val
 Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln
 Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
 Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro
 Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly
 Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
 Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr
 Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg
 Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

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FIG. 86A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTC
GGTTCCTACTGGTGACGTACGGCGAGGGCCCCGGAGCCTGCGGGGCAG
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC
TGCTGGTCCGCCACTGCGTGCCCTGCGGGCTCCTGCGCACGCCGCGGC
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG
CCGCAGGAGTCGGTGGGCGCGGGGGCCGCGCAGGCGGCGGTGACACA
AACTCACACATGCCCCACCGTGCCAGCACCTGAACTCCTGGGGGGA
CCGTCAGTCTTCTCTTCCCCCAAAACCCAAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGA
AGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTCACCCTGTCACCAGGACTGGCTGAATGG
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACG
CCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
CCCTGTCTCCCGGAAATGA

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FIG. 86B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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FIG. 87

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
Asn Leu Glu Gln Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

FIG. 88

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr
Leu Val Thr Val Ser Ala

FIG. 89

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

FIG. 90

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser

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FIG. 91

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
 Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Thr Leu Thr Ile Ser
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
 Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 Ser Phe Asn Arg Gly Glu Cys

FIG. 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
 Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
 Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
 Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
 Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
 Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
 His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

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FIG. 93A

ATGGATTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA
GTCATAATGTCCAGAGGGCAAATIGTTCTCTCCAGTCTCCAGCAATC
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG
CTCAAGTGTAAGTTACATCCACTGGTTCAGCAGAAGCCAGGATCCTC
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC
TGTTGCTTCAGTGCCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT
GGACTAGTAACCCACCCACGTTCTGGAGGGGGGACCAAGCTGGAATC
AAA

FIG. 93B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 94A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG
CCTGGGGCCTCAGTGAAGATGTCTGCAAGGCTTCTGGCTACACATT
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT
GGAATGGATTGGAGCTATTATCCCGGAAATGGTGATACTTCCTACAA
TCAGAAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 94B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ala

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FIG. 95A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAAATAAAA
AAAATTAGTCAGCCATGCATGGGCGGAGAATGGGCGGAACCTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTG
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCCACAGAATTAATTTCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGGCC
ATTGACGTCATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT
TATGGGACTTTTCTACTTGGCAGTACATCTACGTATTAGTACATCGTA
TTACCATGGTGATGCGGTTTGGCAGTACATCAATGGGCGTGGATAGC
GGTTTGACTCAGGGGATTTCGAAGTCTCCACCCCATGACGTCAATG
GGAGTTTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACCTCCGCCCCATTGACGCAAAATGGGCGGTAGCGGTGACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCAGATCTCTCACCATGAGGGTCCCCGCTCAGCTCCT
GGGGTCTCCTGCTCTGGCTCCCAGGTGCACGATGTGATGGTACCAA
GGTGAAAATCAAAACGTACGGTGGCTGCACCATCTGTCTTCATCTCCC
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCT
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACC
ATCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAG
TGTTGAATTAGATCCGTTAACGGTTACCAACTACCTAGACTGGATT
GTGACAACATGCGGCGTGATATCTACGTATGATCAGCCTCGACTGTG
CCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTCCCCCGTGCCTTCT
TGACCCTGGAAGGTGCCACTCCCCTGTCCTTTTCTAATAAAATGAGG
AAATTGCATCGCATTTGTTCTGAGTAGGTGTCATTCTATTCTGGGGGGTG
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG
GCATGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGAC
AGCTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGC
CCGCTTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTACTT
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT
TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGA
TTTCCAAGTCTCCACCCCATGACGTCAATGGGAGTTGTTTGGGCAC

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FIG. 95B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTACAGTGATCAGCACTGAACACAGACCC
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTGCGTGTGTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGCTAGTCTTC
CTCTTCCCCCAAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAGCCCTCCAGCCCCATCGAGAAAACCA
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAGGAACAGGTACGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGGAGAAACAACACAGACCGCTCCCGTGTCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTGCTG
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTGGCCCTCCCCCGTGCCTTCCTTGA
CCCTGGAAGGTGCCACTCCCACTGTCTTCTCAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGG
TGGGCGAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCAAGCTGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTGTCTTCTCAATTCTTATTGTCATA
ATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTGAGTAGTTGAT
TGAGCAAAATGCGTTGCCAAAAAGGATGCTTAGAGACAGTGTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATACCCGAAGCCTGATTCCGTAGAGCCACACCTTGTTAAGGGCC
AATCTGCTACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCAATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 95C

GCTGCGATTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTTGAAGTGCAT
CGTCGCCGTGTCCAAAAATATGGGGATTGGCAAGAACGGAGACCTAC
CCTGGCCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC
ACAACTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG
GAAAACCTGGTTCTCCATTCTTGAGAACATCGACCTTTAAAGGACA
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACACCACGAGGA
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT
CTTTGTGACAAGGATCATGCAGGAATTTGAAAAGTGACACGTTTTTCCC
AGAAATTGATTTGGGGAAATATAAACTTCTCCAGAATACCCAGGCG
TCCTCTCTGAGTCCAGGAGGAAAAAGGCATCAAGTTATAAGTTGAA
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTCAAGTTCTCTGC
TCCCCTCCTAAAGTCATGCATTTTATAAGACCATGGGACTTTTGCTG
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTGT
TTGCCCTCCCCCGTGCCTTCTTGACCTGGAAGGTGCCACTCCCAC
TGTCTTTCTCATAAATAAATGAGGAAATTCATCGCATTTGTCTAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT
ATGGAACCAAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT
ATTTGCATAATTGAGAAAAAAGGAAAAATTAATTTAACACCAATTCA
GTAGTTGATTGAGCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACA
GTGTCTCTGCACAGATAAGGACAAACATTATTACAGAGGGAGTACCC
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCATTTAGGGAGA
AATATGCTTGTCATCACCGAAGCCTGATTCGCTAGAGCCACACCTGG
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGCGAGGACGAGG
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC
GGCTATGACTGGGACAAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGA
CCTGTCCGGTGCCCTGAATGAAGTGCAGGACGAGGCAGCGCGGCTAT
CGTGGCTGGCCACGACGGGCGTTCTTGGCGCAGCTGTGCTCGACGTTG
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG
CAGGATCTCCTGTCTCTCACCTTGCTCCTGCCGAGAAAGTATCCATC
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
CCATTGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCG
GATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATC
AGGGGCTCGCGCCAGCCGAACCTGTTCCGAGGCTCAAGGCGCGCATG
CCCACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTCCG

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FIG. 95D

AATATCATGGTGGAAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGT
GCTTACGGTATCGCCGCTTCCGATTTCGACGCGCATCGCCCTTCTATC
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGAC
CGACCAAGCGACGCCCCAACC TGCCATCAGGAGATTTTCGATTCCACCG
CCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTCCGGGACGCCG
GCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCC
ACCCCAACTTGTTTATTGACGCTTATAATGGTTACAAATAAAGCAATA
GCATCACAATTTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT
GTGGTTTGTCACAACTCATCAATCTATCTTATCATGTCTGGATCGCGG
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC
TGTGTGAAATTGTTATCCGCTCACAAATCCACACAACATACGAGCCGG
AGCATAAAGTGTAAGCCCTGGGGTGCCCTAATGAGTCGATTCACTAC
ATTAATTGCGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTC
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCGTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTC
GGTCGTTCCGGTCGCGGAGCGGTATCAGCTCACTCAAAGGCGGTAA
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC
TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCGTATCCGACC
CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG
GCGCTTCTCAATGTCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
GTTCTGCTTCAAGCTGGGCTGTGTACGAACCCCCCGTTACCGCCGAC
CGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTCCAACCGGTAAGA
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA
AGCCAGTTACCTTCGGAAAAAAGAGTTGGTAGCTCTGATCCGGCAAA
CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAGAACTGGATTT
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
GGGCTTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG
TCATGAGATTATCAAAAAAGGATCTTCACTAGATCCTTTTAAATTA
AATGAAGTTTTAAATCAATCTAAAGTATATAGATAAACTTGGTCTG
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC
TATTTCTGTTATCCATAGTTGCCTGACTCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC
GAGACCCACGCTACCGCTCCAGATTTATCAGCAATAAACACGCCA
GCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCG

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FIG. 95E

CAGTTAATAGTTTGC GCAACGTTGTTGCCATTGCTACAGGCATCGTGG
TGTCACGCTCGTCGTTTGGIATGGCTTCATTCAGCTCCGGTTCCCAAC
GATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCCTCCGATCGTTGT CAGAAGTAAGTTGGCCGCAGTG
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAA
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC
ATTGGAAAACGTTCTTCGGGGCGAAAAC TCTCAAGGATCTTACCGCTG
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCA
GCATCTTTTACTTTACCCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAATGTTGAA
TACTCATACTCTTCTTTTCAATATTATTGAAGCATTATCAGGGTTA
TTGTCTCATGAGCGGATACATATTTGAATGTATTAGAAAAATAAAACA
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

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FIG. 96A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACCTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAAGTGA
CACACATTCCACAGAAATTAATCCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGGTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCT
TATGGGACTTTCTACTTGGCAGTACATCTACGTTAGTCAATCGTGA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCCATTGACGTCAATG
GGAAGTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAAATGTCGTA
ACAACCTCCGCCCATTTGACGCAAAATGGGCGGTAGCCGCAATAGGGA
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT
CAGCTTCTCTGTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT
TGTTCTCTCCCACTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA
GGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATCCACT
GGTTCCAGCAGAAGCCAGGATCCTCCCCCAAACCTGGATTTATGCCA
CATCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGT
CTGGGACTTCTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAAGCCACCCACGTCG
GAGGGGGGGACCAAGCTGGAATCAAACGTACGGTGGCTGCACCATCT
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCC
TCTGTTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
CAGTGAAGGTGGATAACGCCCTCCAATCGGTAAGTCCCAGGAGAG
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACAAAAAGTCTACGCC
TGCGAAGTCAACCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT
CAACAGGGGAGAGTGTGAATTCAGATCCGTTAACGGTTACCAACTA
CCTAGACTGGATTCTGTGACAACATGCGGCCGTGATATCTACGTATGAT
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGGCCCTC
CCCCGTGCCTTCTTGACCTGGAAGGTGCCACTCCCACTGTCCTTTCC

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FIG. 96B

TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA
GCTGGGGCTCGACGCTATGCCAAGTACGCCCCCTATTGACGTCAATG
ACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT
GGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTG
ACTACGGGGATTTCCAAAGTCTCCACCCCATTGACGTCAATGGGAGTT
TGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACT
CCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC
TATATAAGCAGAGCTGGGTACGTCTCACATTCAGTGATCAGCACTGA
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT
CGCTGTTGTACGCGTGTCTGTCCAGGTACAACCTCAGCAGCAGCTGG
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAACAGA
CACCTGGTCCGGGCTGGAATGGATTGGAGCTATTTATCCCGGAAAT
GGTGATACCTTCTACAATCAGAAGTCAAAGGCAAGGCCACATTGAC
TGCAGACAAATCCTCCAGCACAGCCTACATGCAAGCTCAGCAGCTGA
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTACC
GTCTCTGCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
TCCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTACAGGCG
CCCTGACCAGCGGCGTGCACACCTTCCCGGTGTCTACAGTCTCTAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCAAGCCAGCAACACC
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGCAAAAACCTCACAC
ATGCCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT
CCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCC
TGAGGTCAACATGTCGTGGTGGTGGAGCTGAGCCACGAAGACCCGTAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGAGTATGCGCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCC
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAGGTGTACACCCT
GCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACGCTGACCT
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG
AGCAATGGGACGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGTCT
GGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGCTTCTCATGTCTCCGTGATGCGATG
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGT

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FIG. 96C

GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG
ACCCCTGGAAGGTGCCACTCCCACTGTCTTTCTTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC
ATGCTGGGGATGCGGTGGGCTCTATGGAACCACTGGGGCTCGACAG
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTCAT
AATGAGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGA
TTGAGCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCT
GCACAGATAAGGACAAACATTATTTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCTACACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTCGCATTCG
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC
CCCGCTGCCATCATGGTTTCGACCATTTGAAGTGCATCGTCGCGGTGTC
CAAAATATGGGATTGGCAAGAACGGAGACCTACCTGGCCCTCCGCT
CAGGAACGAGTTCAGTACTTCCAAAGAATGACCACAACTCTTCAG
TGGAAGGTAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC
TCCATTCTGAGAAGAAATCGACCTTTAAAGGACAGAATTAATATAGTT
CTCAGTAGAGAACTCAAAGAACCACGAGGAGCTCATTTTCTTGC
CAAAAGTTTGGATGATGCCCTTAAGACTTATGGAACCCGGAATTGG
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTCTGTTTACC
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG
ATCATGCAGGAATTTGAAAAGTGACACGTTTTTCCAGAAATTGATTG
GGGAAATATAAACTTCTCCAGAATACCCAGGCGTCTCTGA
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCCTCTAA
AGCTATGCATTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA
GCCTCGACTGTGCCCTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCC
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACCTGCTTCTTA
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCTTCTAT
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCACT
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTATTGTCATAATG
AGAAAAAAGGAAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA
GCAAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTCTCTGCA
CAGATAAGGACAAACATTATTTCAGAGGGAGTACCCAGAGCTGAGACT
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTG
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

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FIG. 96D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTG
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC
AGCGCAGGGGCGCCCGTTCTTTTGTCAAAGACCGACCTGTCCGGTGC
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA
CGACGGGCGTTCTTGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
TCATCTCACCTTGCTCCTGCGGAGAAAGTATCCATCATGGCTGATGCA
ATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAC
CAAGCGAAACATCGCATCGAGCGAGCACGTA CTGGATGGAAGCCGG
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC
CAGCCGAAC TGTTCCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAG
GATCTCGTCGTGACCCATGGCGATGCCGTGCTTGCCGAATATCAGCCG
GAAAATGGCCGCTTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTAT
CGCCGCTCCGATTCTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGCA
GCCAACCTGCCATCACGAGATTTGATTCCACCGCCGCTTCTATGA
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCAACTTGTT
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTGTCCAA
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATGTT
TATCCGCTCACAATTTCACACAACATACGAGCCGGAAGCATAAAGTG
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT
GCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTGCTGCCAGCTGCA
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGC
GCTCTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCCGGCT
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA
CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC
ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACACGGCTTTC
CCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTAC
CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAA
GCTGGGCTGTGTGCACGAACCCCGGTTACGCCGACCGCTGCGCCTT
ATCCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

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FIG. 96E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGC
TGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAA
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
TCAGTGGAAACGAAAACCTCACCTAGATCCTTTAAATAAAAATGAAGTTTAA
AAAAAGGATCTTCACCTAGATCCTTTAAATAAAAATGAAGTTTAA
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
CTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCG
AGCGCAGAAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTA
ATTGTTGCCGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGT
TTGGTATGGCTTCATTAGCTCCGGTTCCCAACGATCAAGGCGAGTTA
CATGATCCCCCATGTTGTGCAAAAAAGCGTTAGCTCCTTCGGTCCTC
CGATCGTTGTCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTA
TGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT
TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
TGCGGCGACCGAGTTGCTCTTGCCCGCGTCAATACGGGATAATACC
GCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCT
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTTCG
ATGATACCCACTCGTGCACCCAACCTGATCTTCAGCATCTTTTACTTTCA
CCAGCGTTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAA
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT
TTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGACGG
ATACATATTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCGCG
GCACATTTCCCGAAAAAGTGCCACCT

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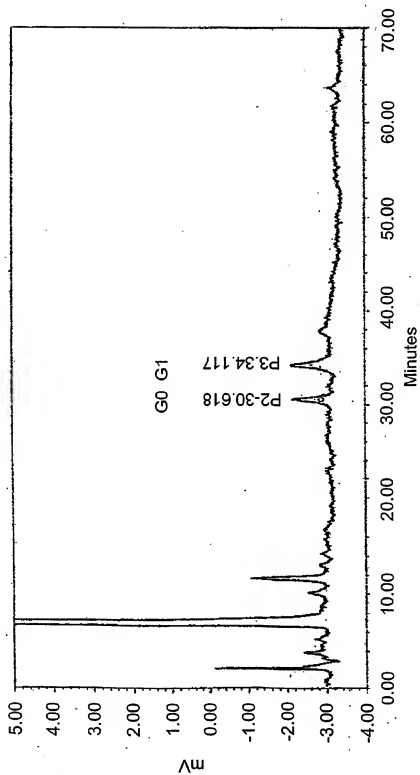


FIG. 97A

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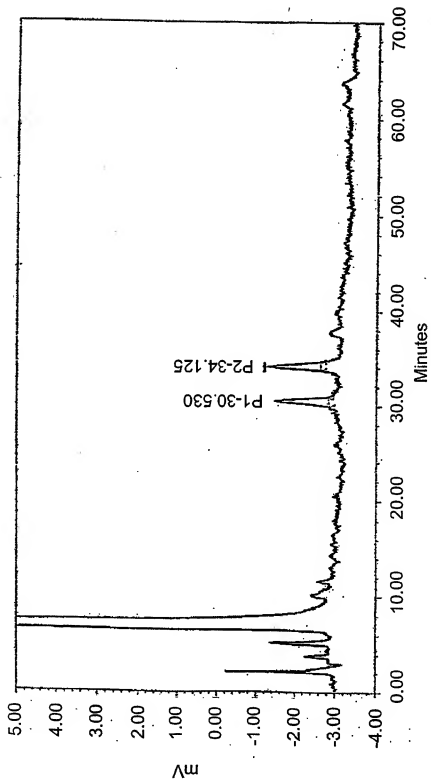


FIG. 97B

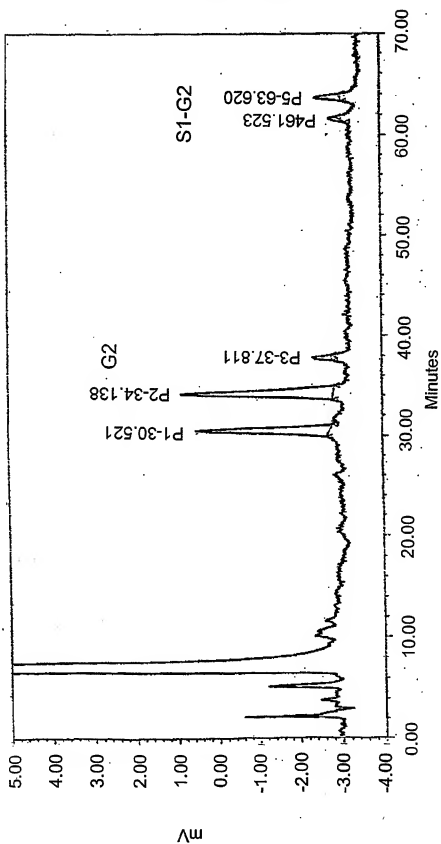


FIG. 97C

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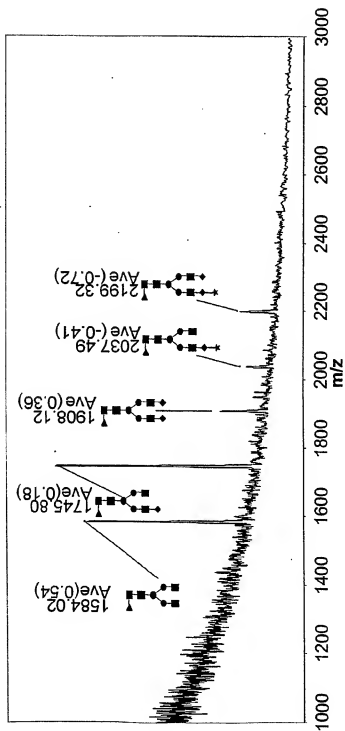


FIG. 98A

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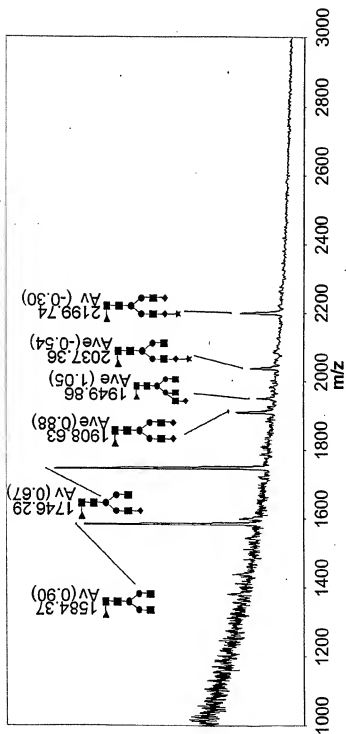


FIG. 98B

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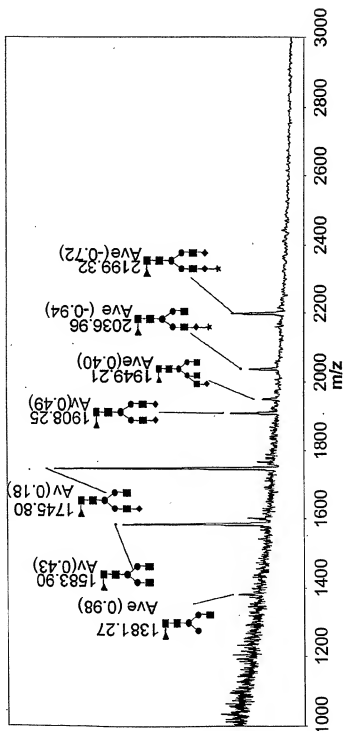


FIG. 98C

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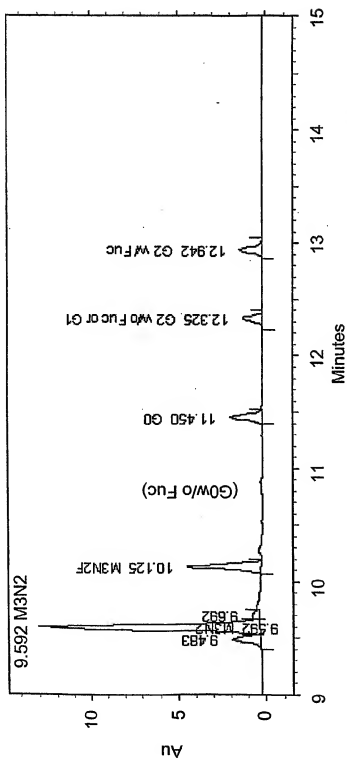


FIG. 99A

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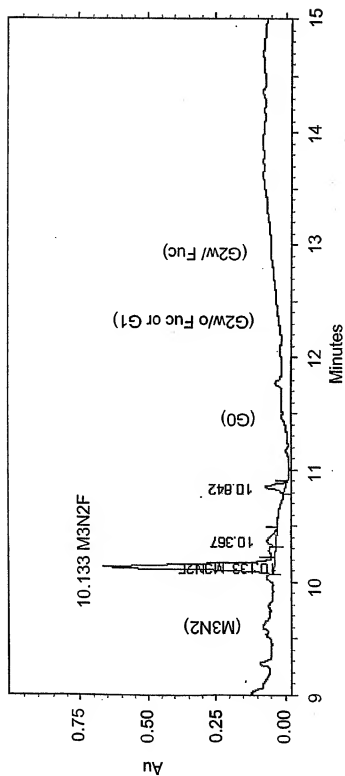


FIG. 99B

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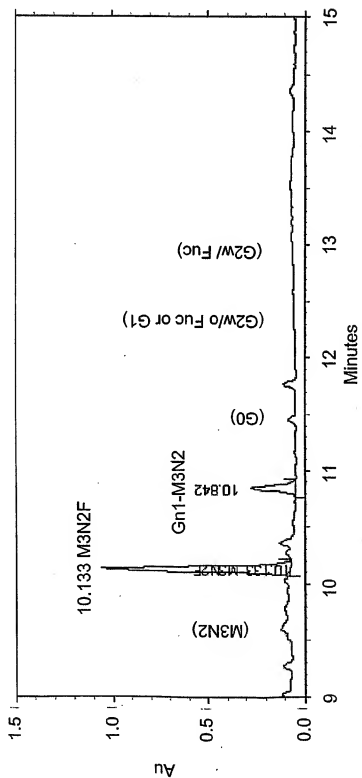


FIG. 99C

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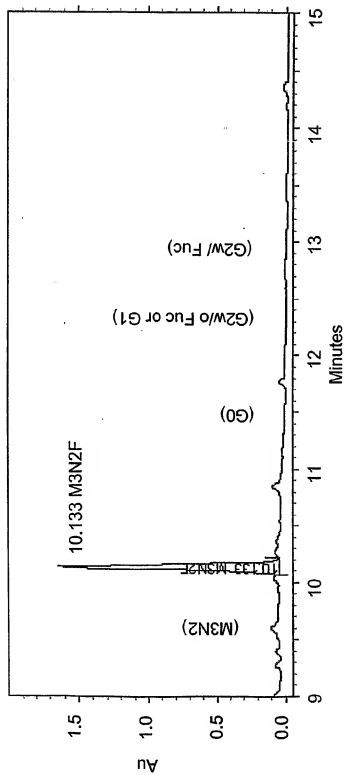


FIG. 99D

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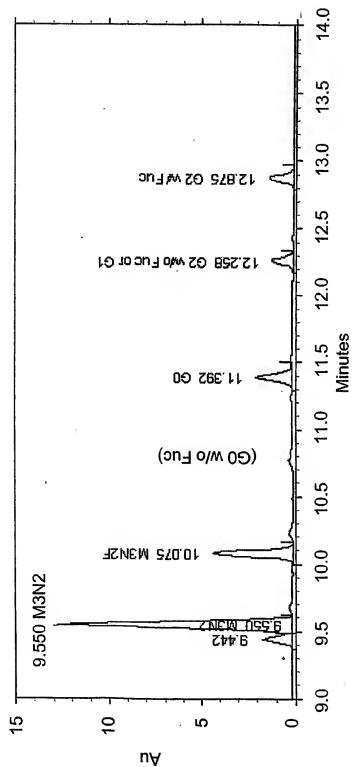


FIG. 100A

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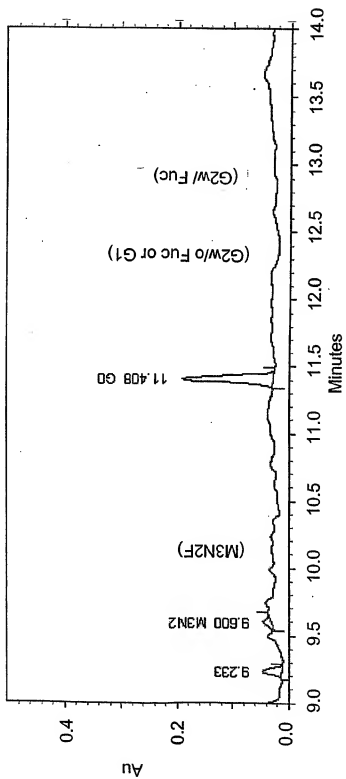


FIG. 100B

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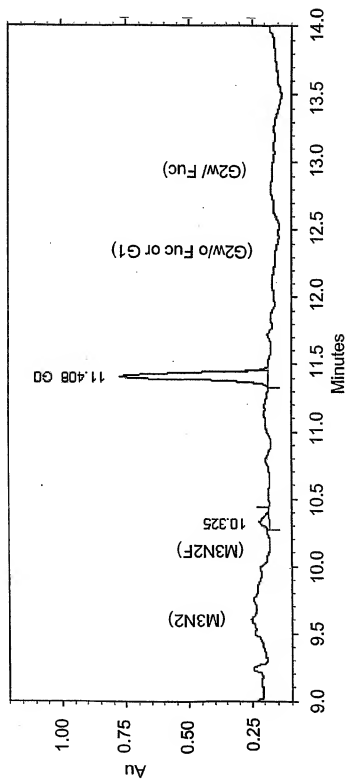


FIG. 100C

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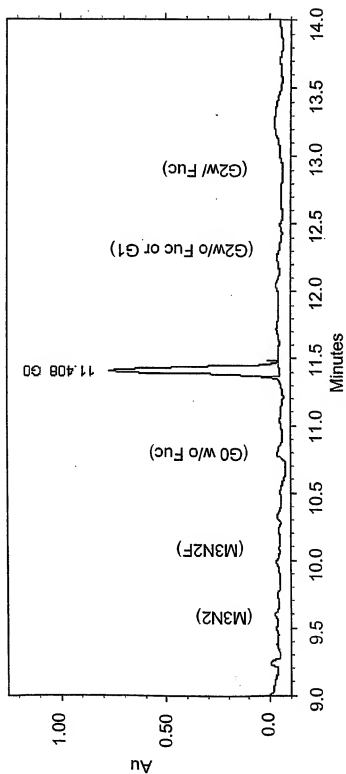


FIG. 100D

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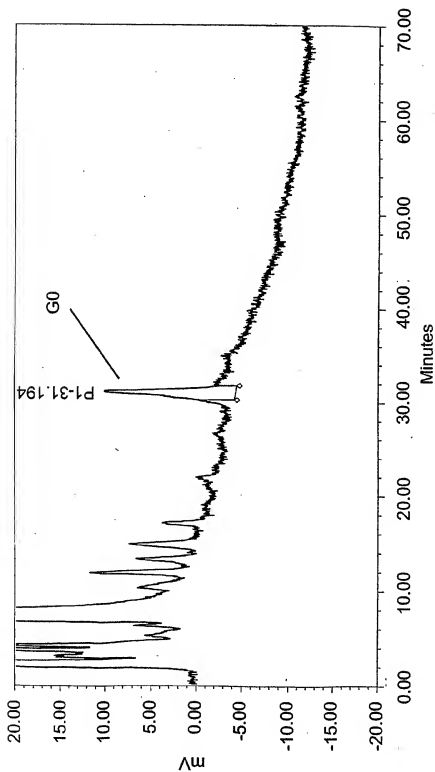


FIG. 101A

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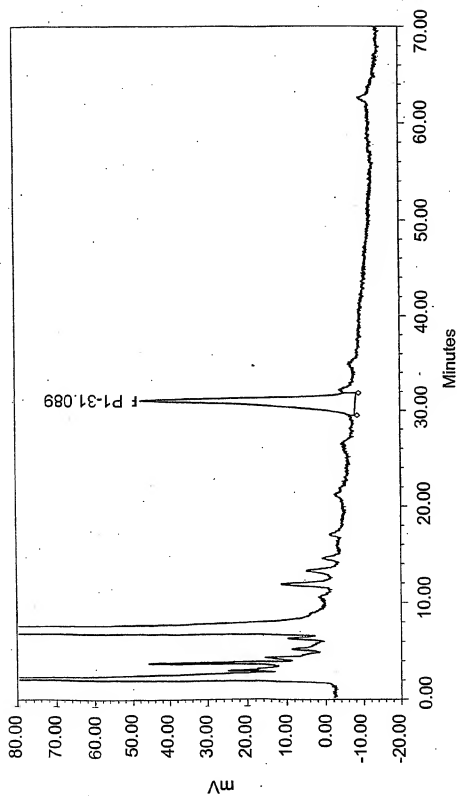


FIG. 101B

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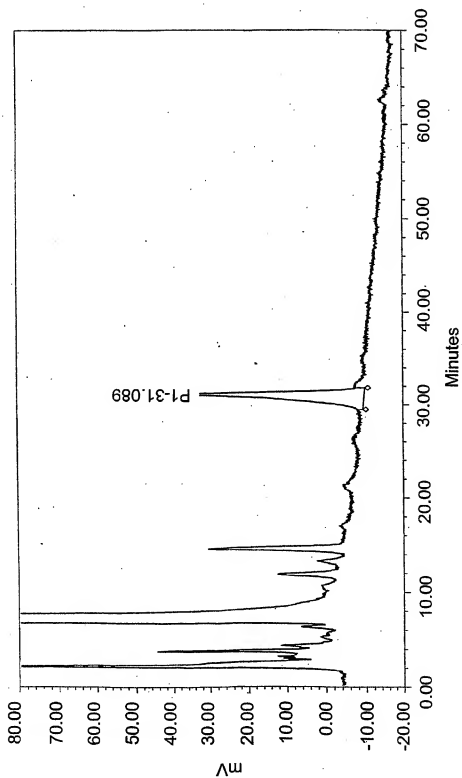


FIG. 101C

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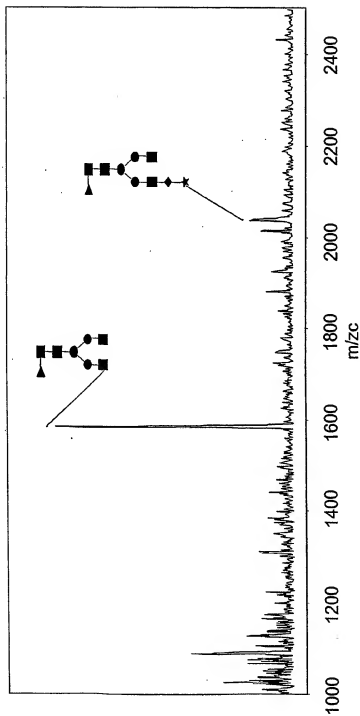


FIG. 102A

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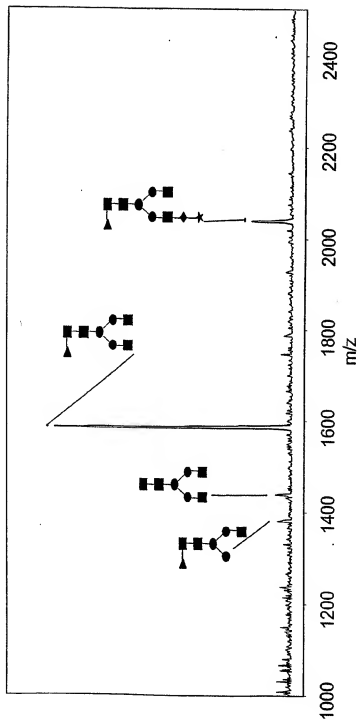


FIG. 102B

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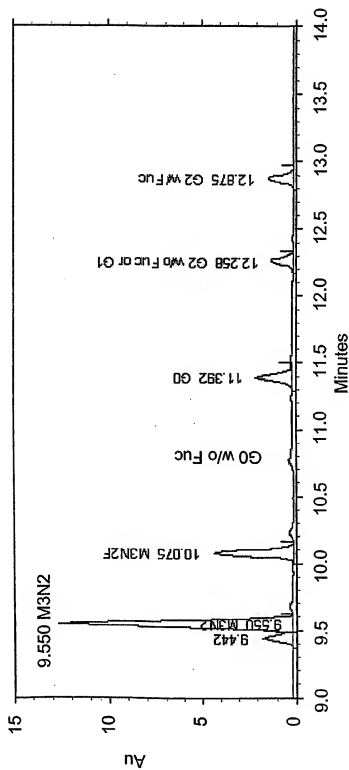


FIG. 103A

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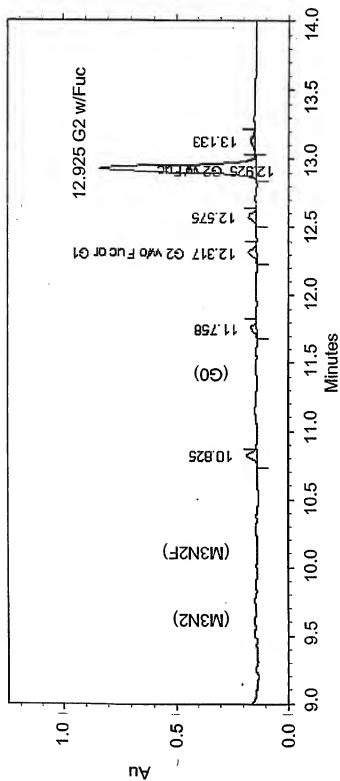


FIG. 103B

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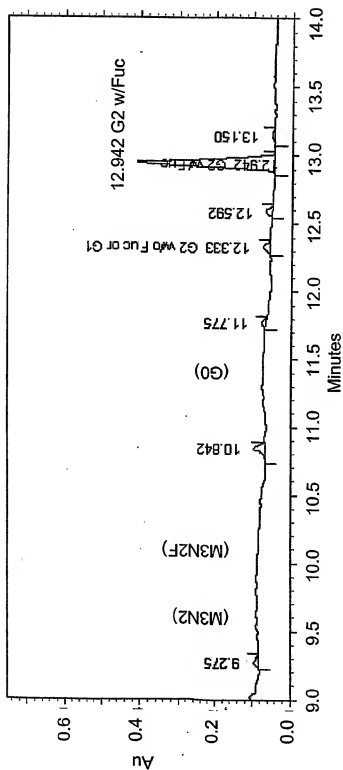


FIG. 103C

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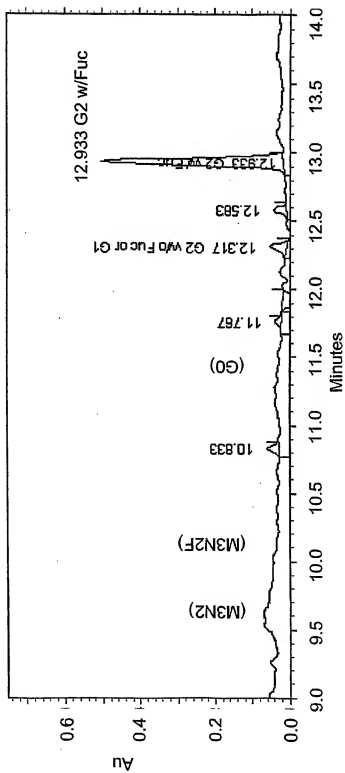


FIG. 103D

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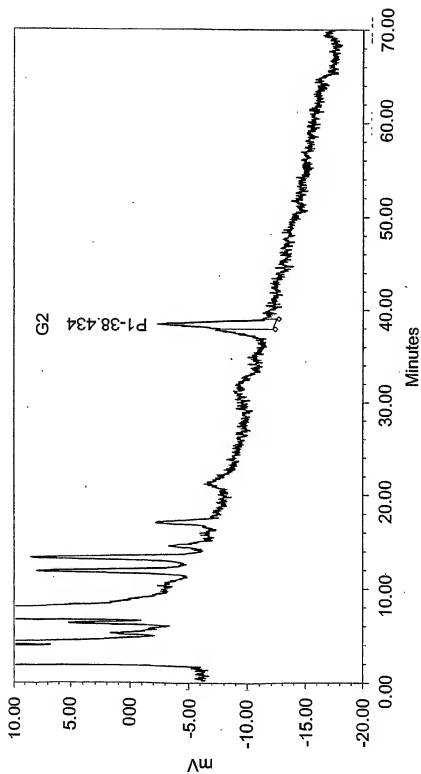


FIG. 104A

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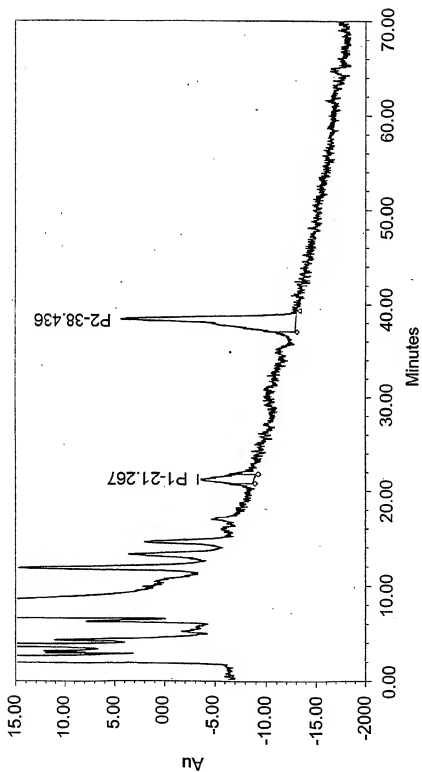


FIG. 104B

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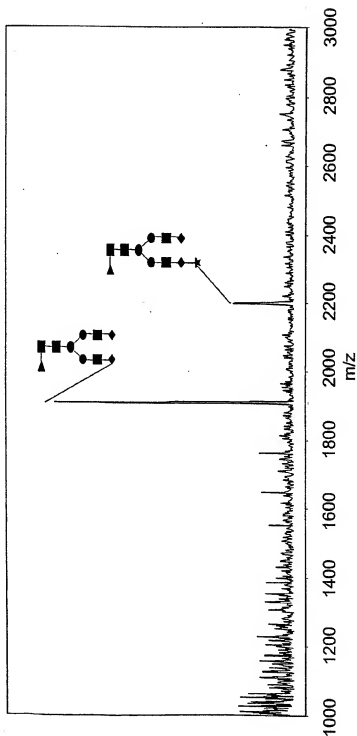


FIG. 105A

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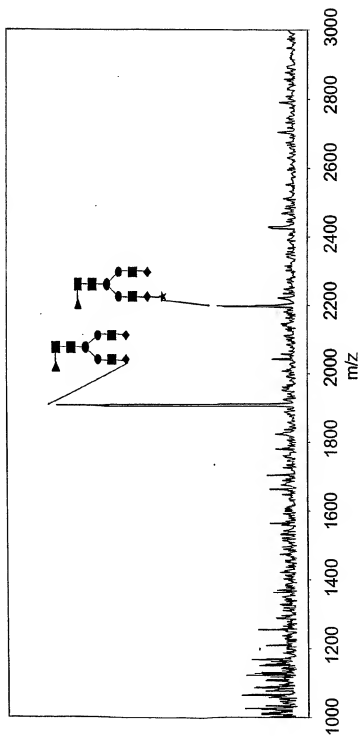


FIG. 105B

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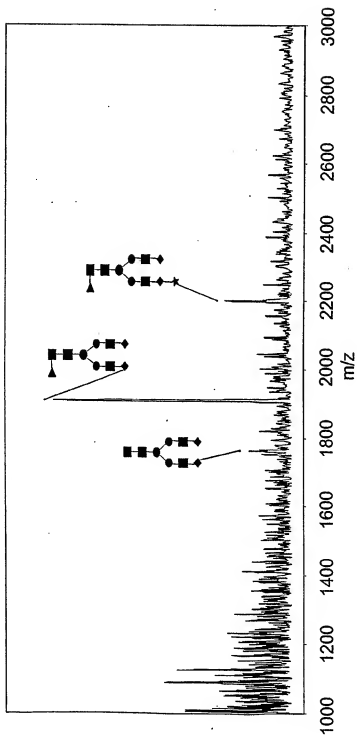


FIG. 105C

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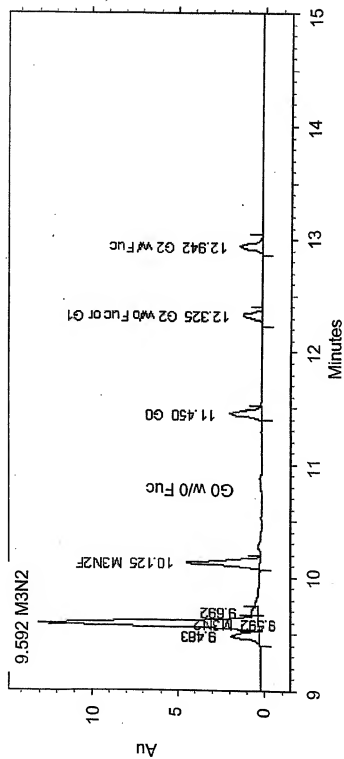


FIG. 106A

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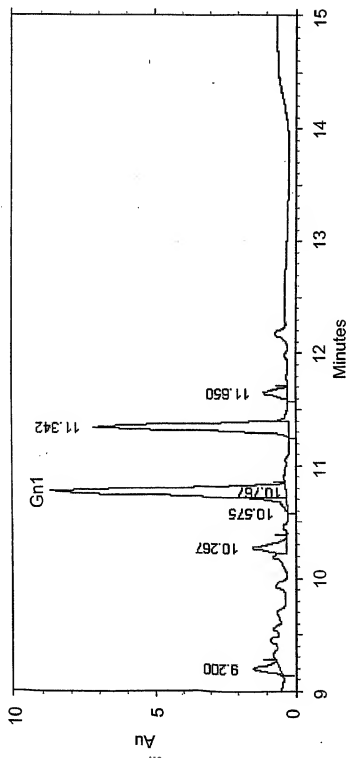


FIG. 106B

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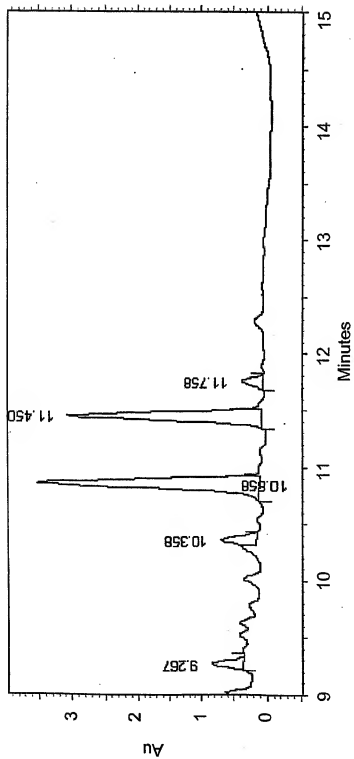


FIG. 106C

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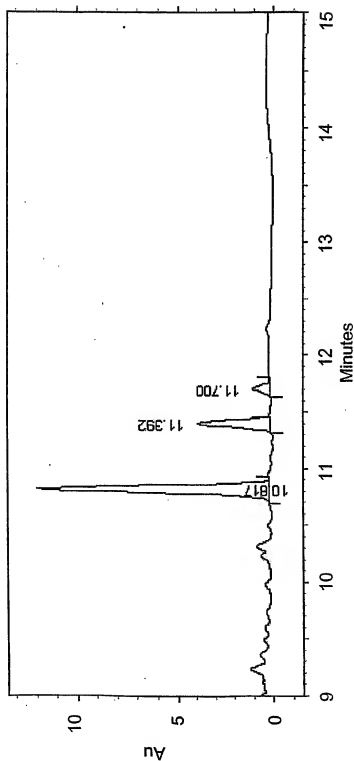


FIG. 106D

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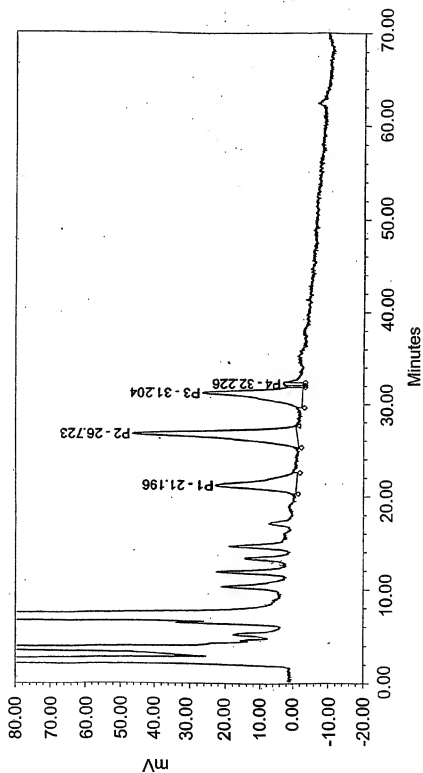


FIG. 107A

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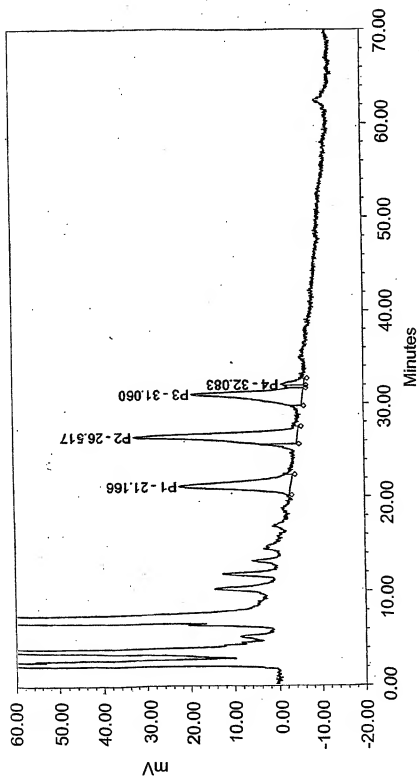


FIG. 107B

379/498

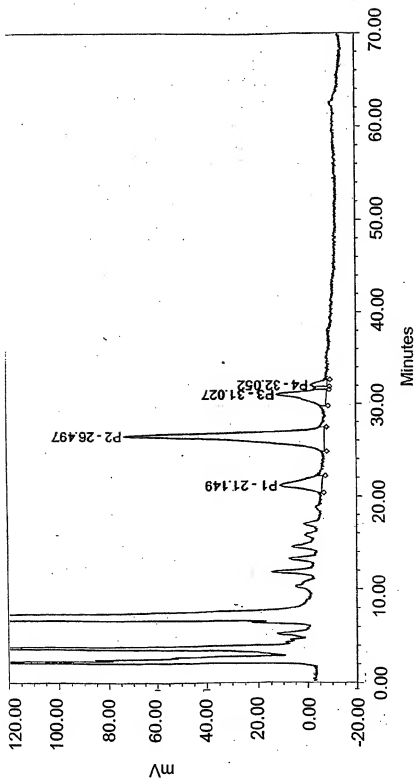


FIG. 107C

380/498

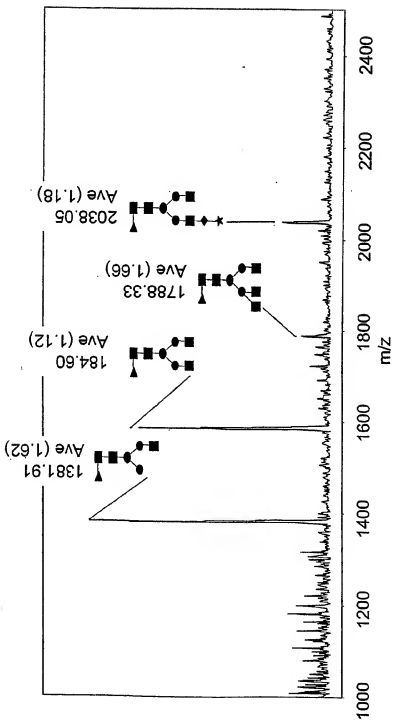


FIG. 108A

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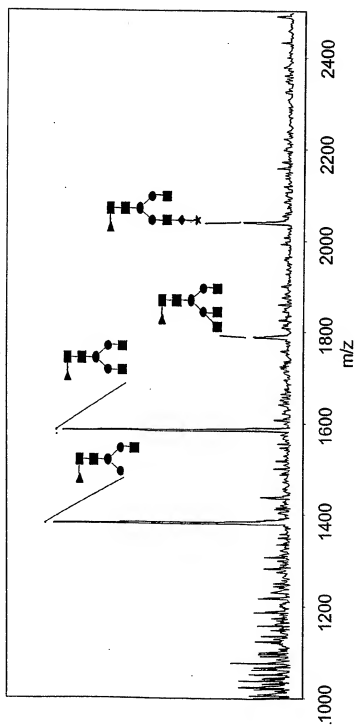


FIG. 108B

382/498

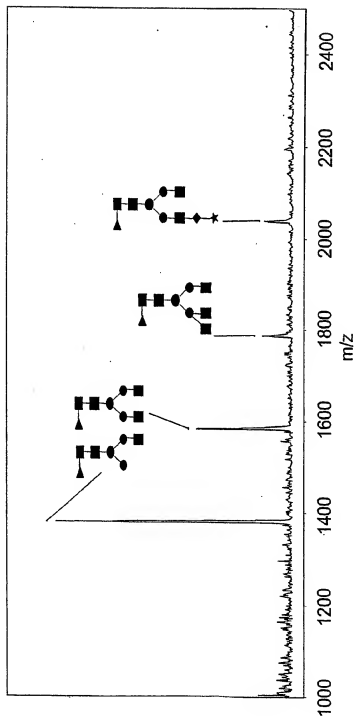


FIG. 108C

383/498

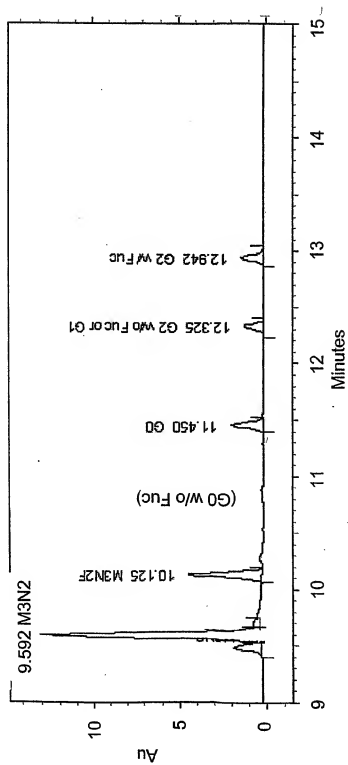


FIG. 109A

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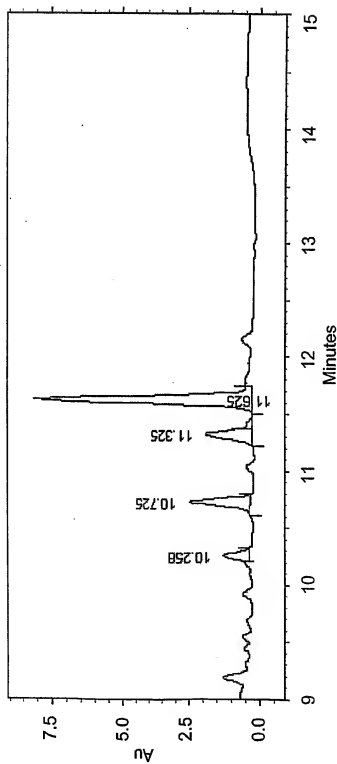


FIG. 109B

385/498

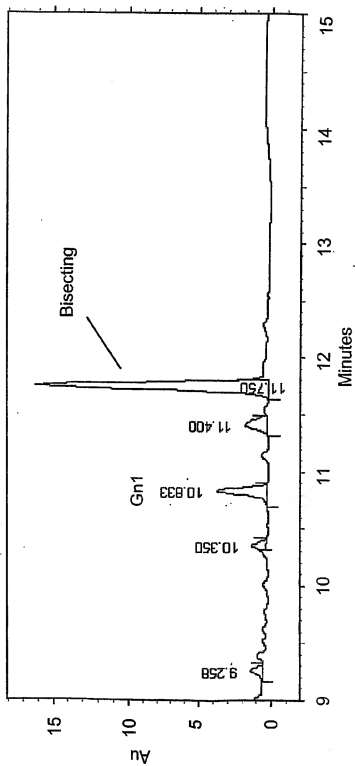


FIG. 109C

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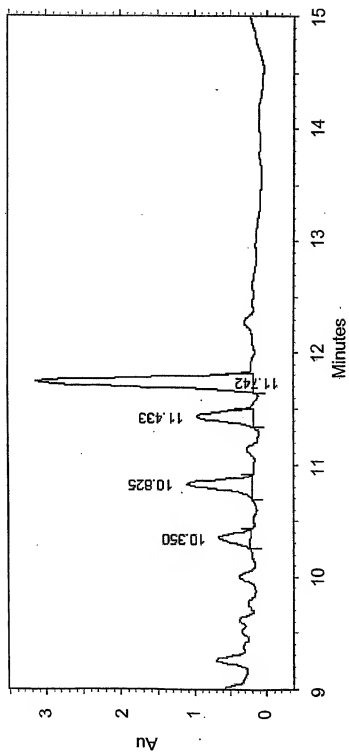


FIG. 109D

387/498

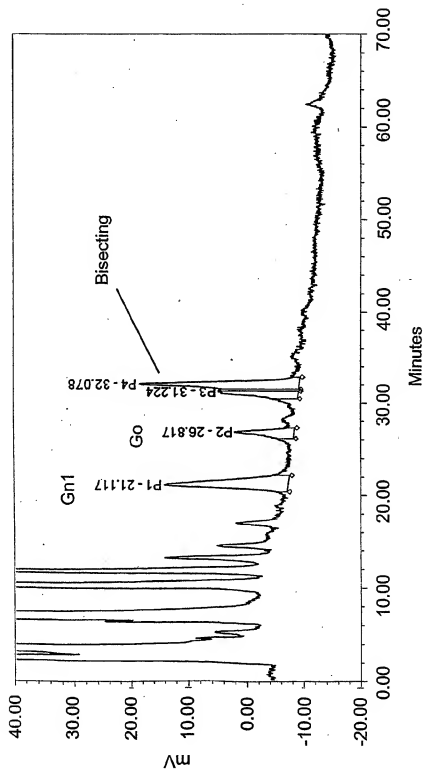


FIG. 110A

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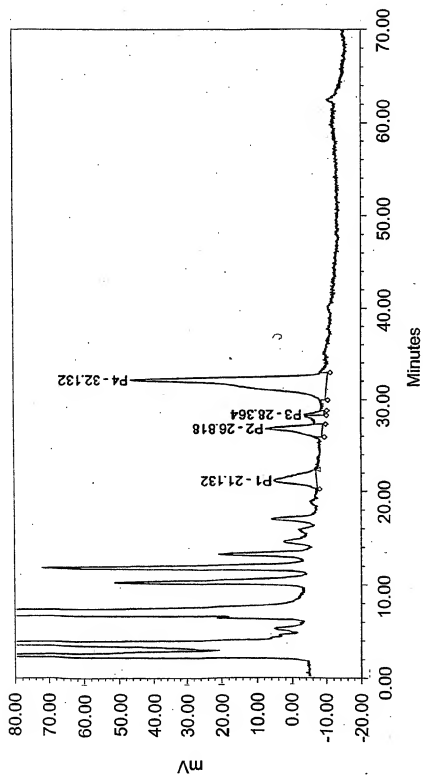


FIG. 110B

389/498

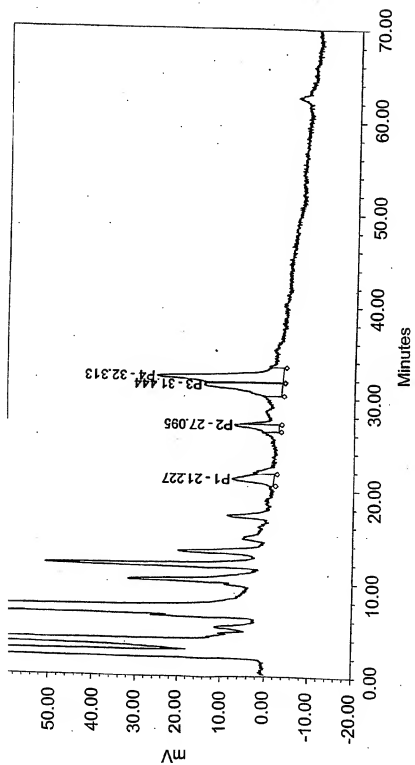


FIG. 110C

390/498

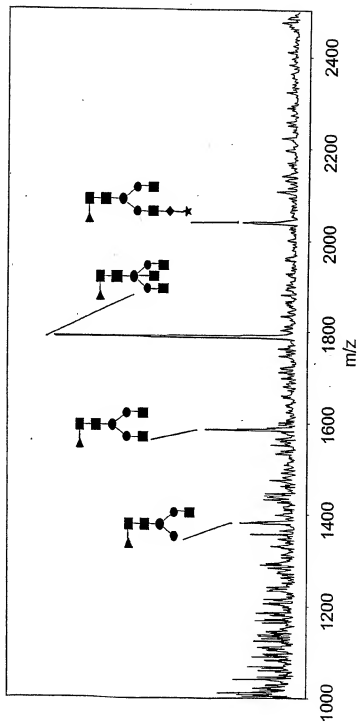


FIG. 111A

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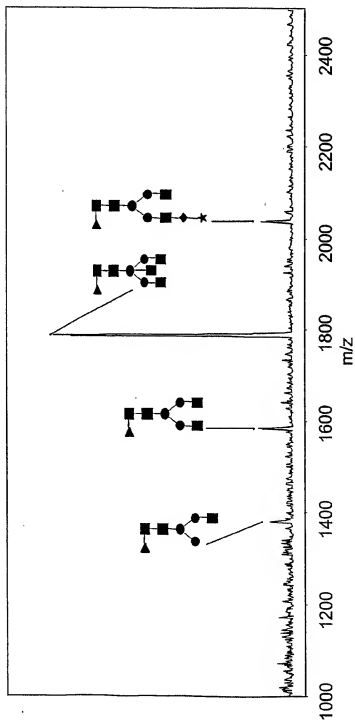


FIG. 111B

392/498

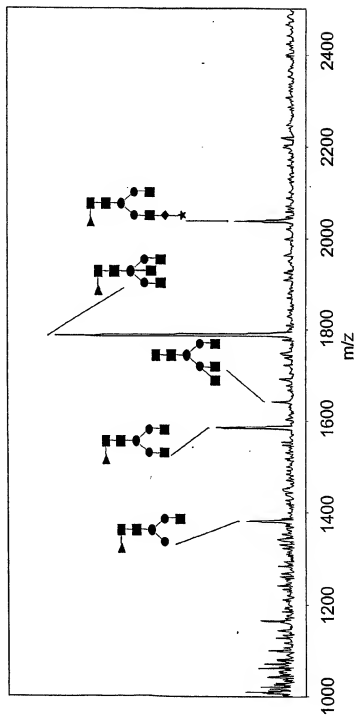


FIG. 111C

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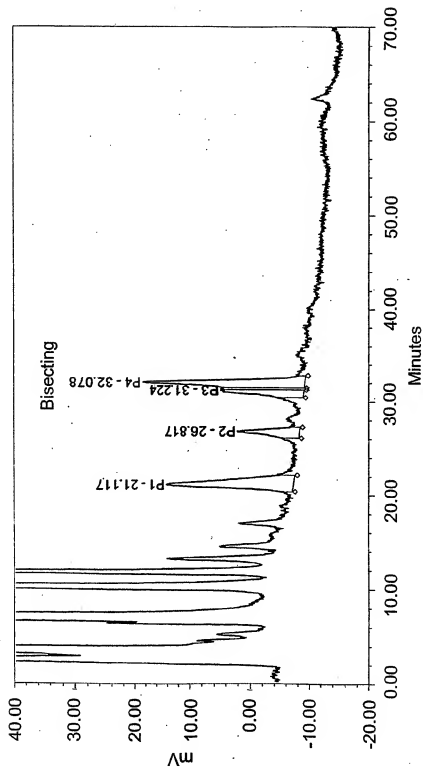


FIG. 112A

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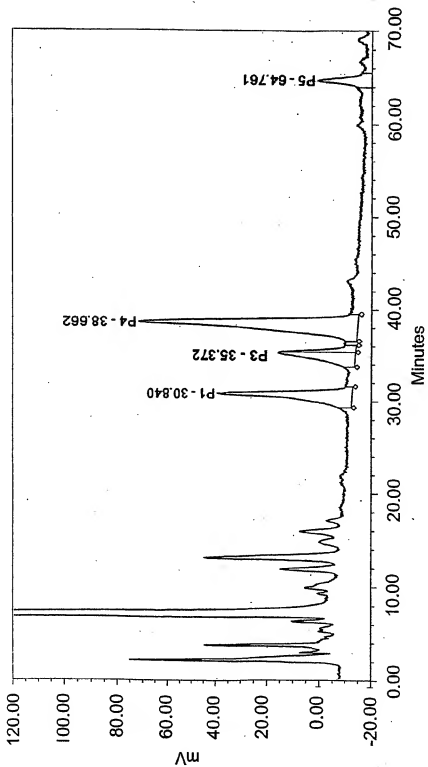


FIG. 112B

395/498

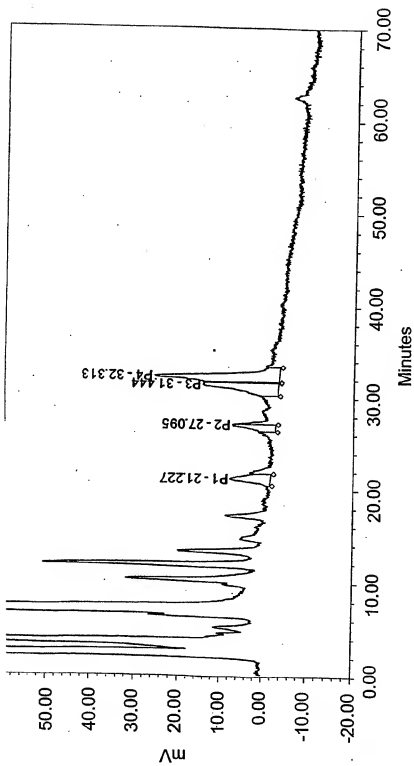


FIG. 112C

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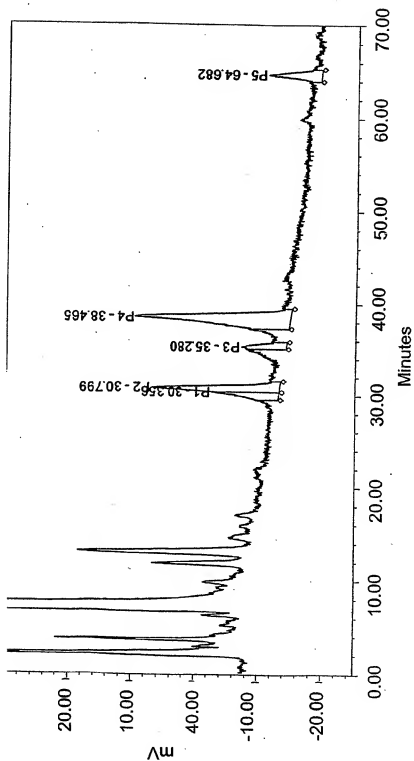


FIG. 112D

397/498

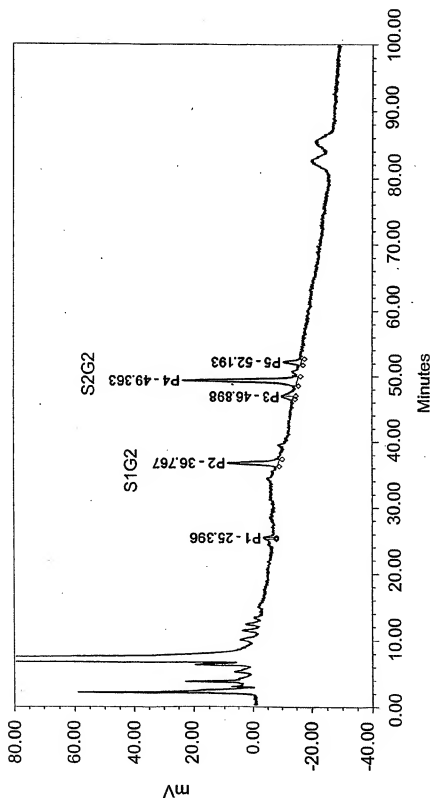


FIG. 113A

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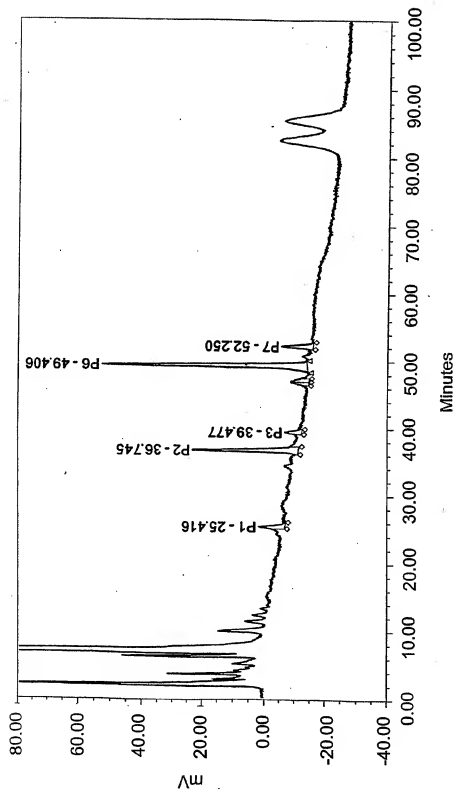


FIG. 113B

399/498

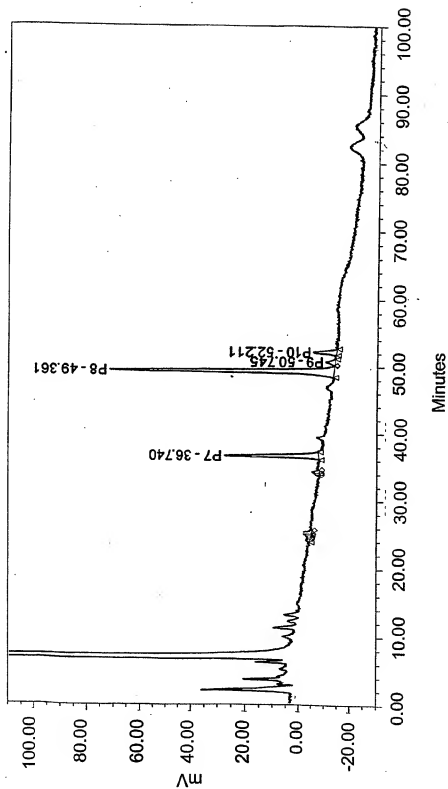


FIG. 113C

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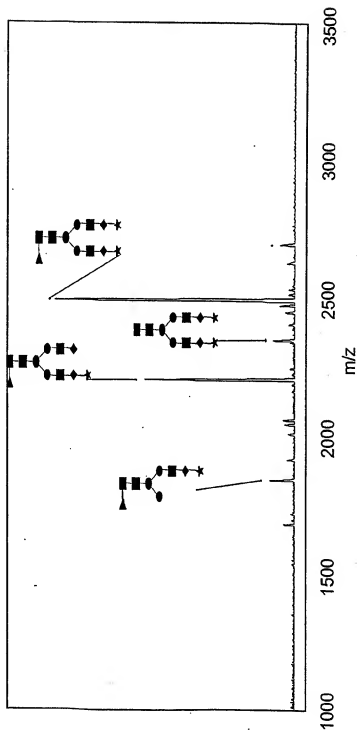


FIG. 114A

401/498

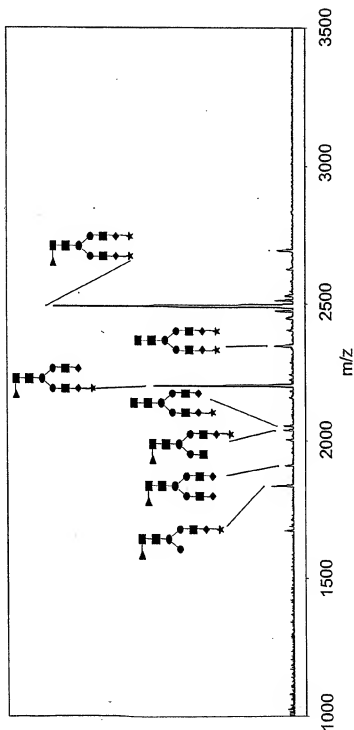


FIG. 114B

402/498

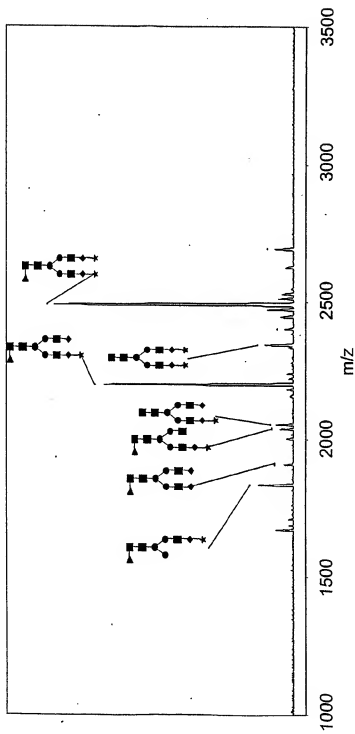


FIG. 114C

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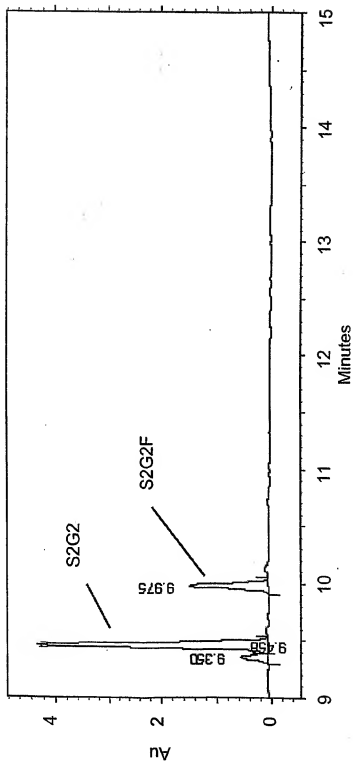


FIG. 115A

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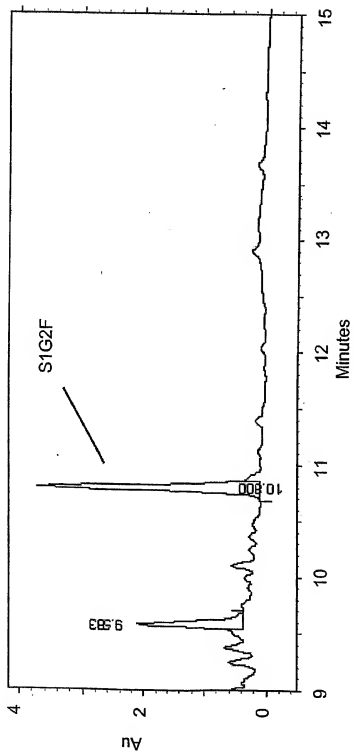


FIG. 115B

405/498

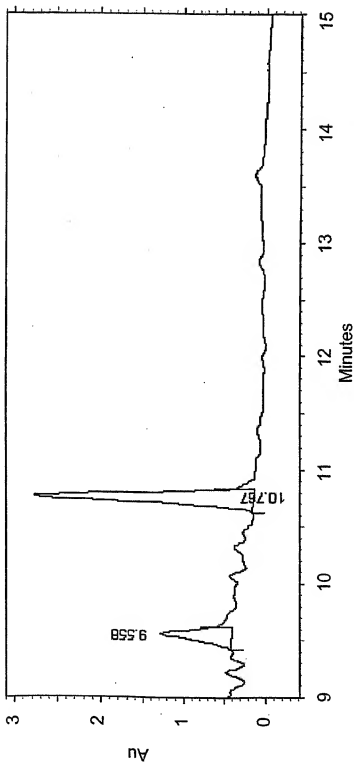


FIG. 115C

406/498

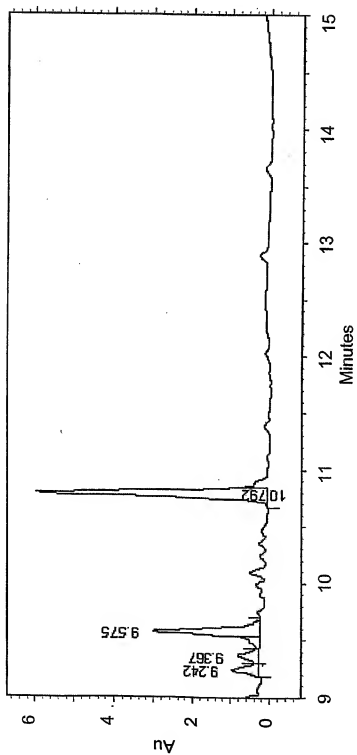


FIG. 115D

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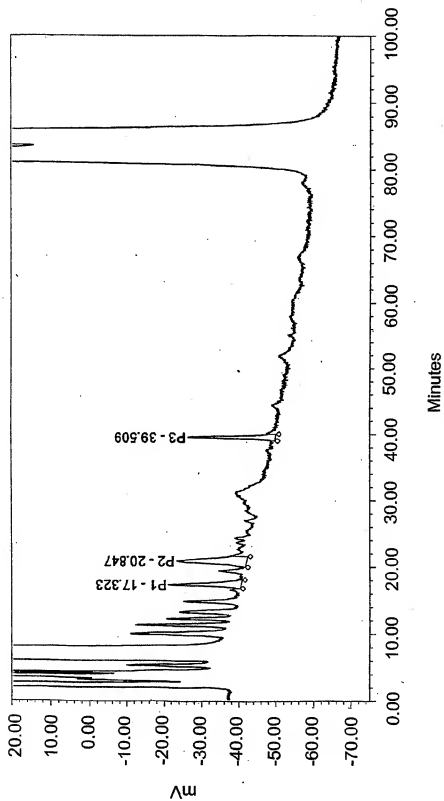


FIG. 116A

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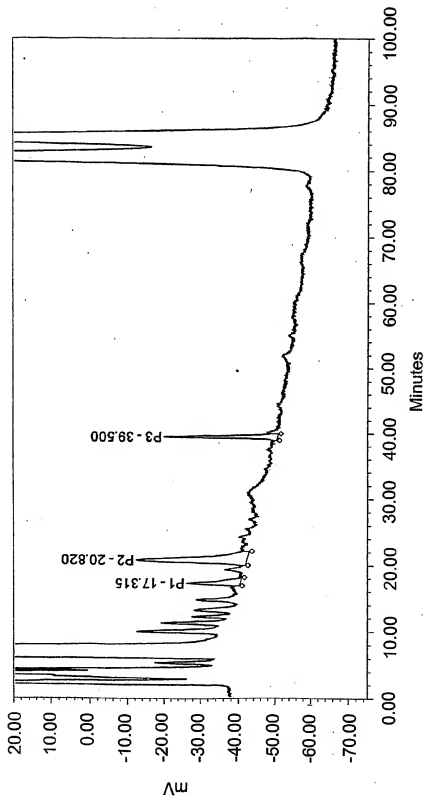


FIG. 116B

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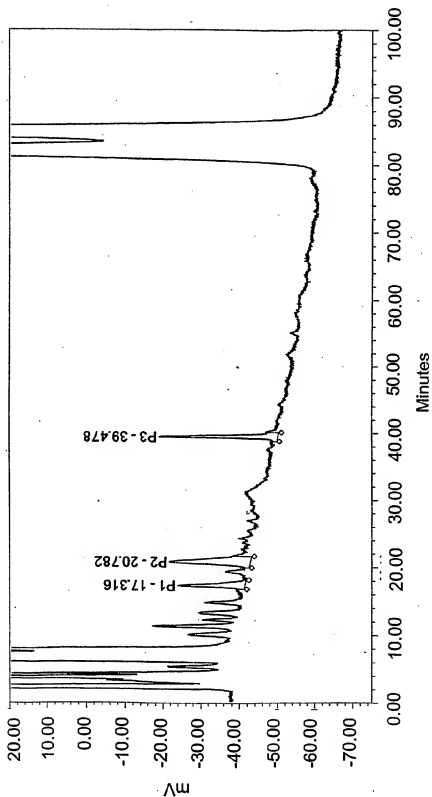


FIG. 116C

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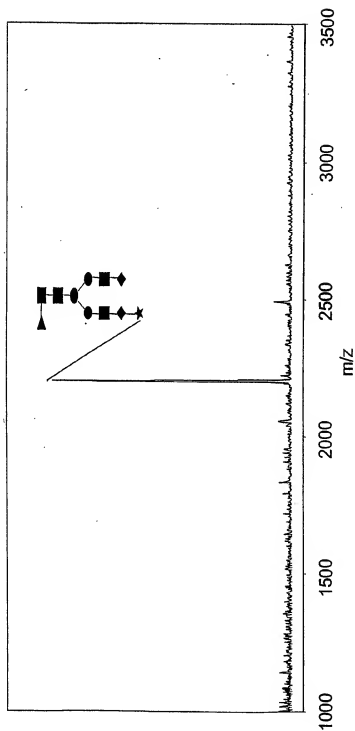


FIG. 117A

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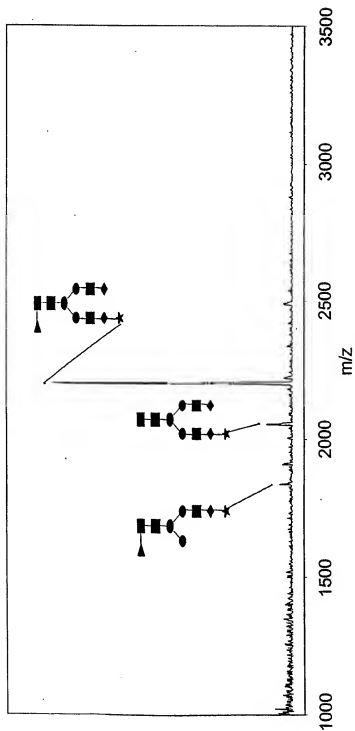


FIG. 117B

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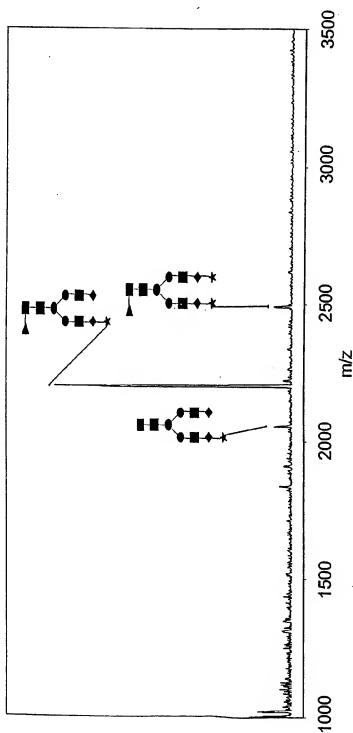


FIG. 117C

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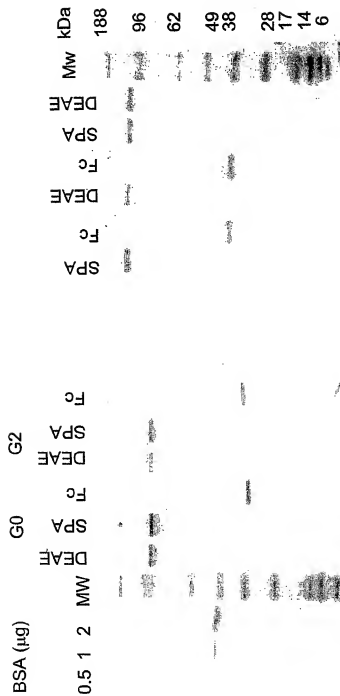


FIG. 118B

FIG. 118A

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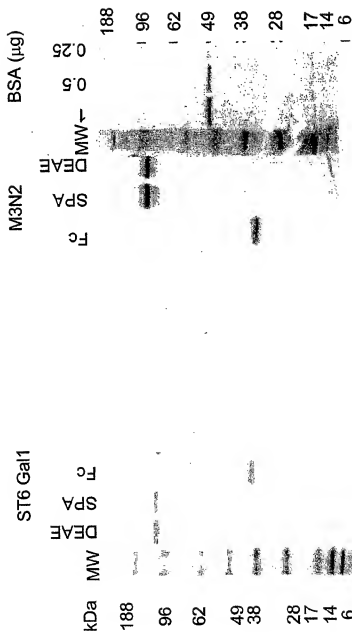


FIG. 118D

FIG. 118C

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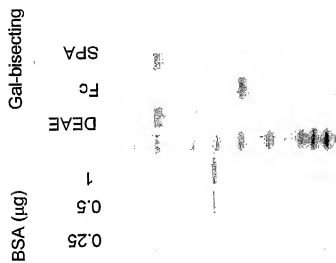


FIG. 118E

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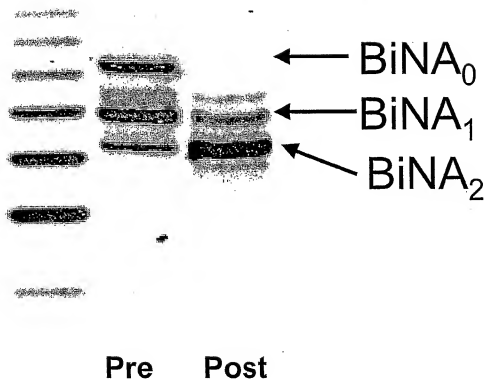


FIG. 119

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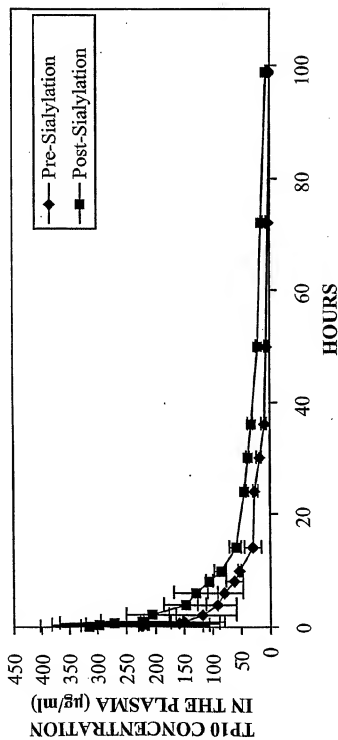


FIG. 120

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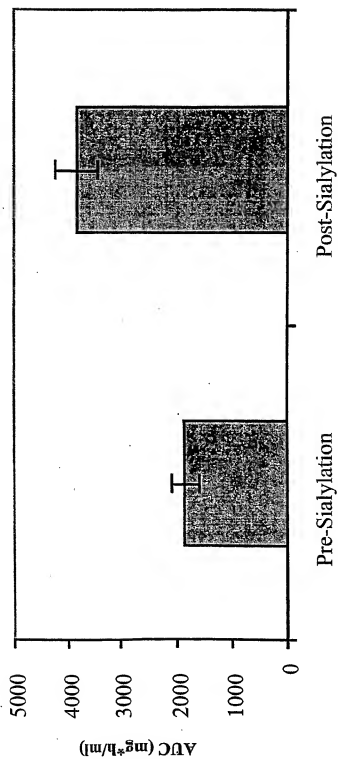


FIG. 121

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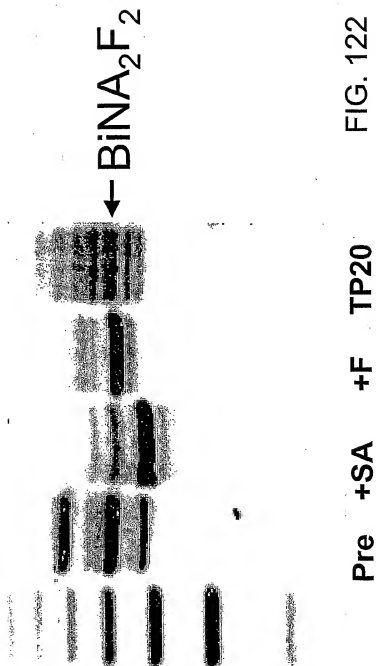


FIG. 122

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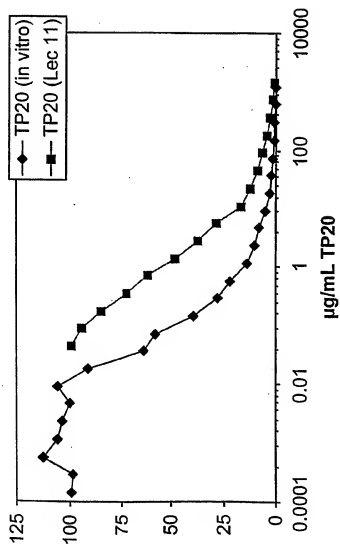


FIG. 123

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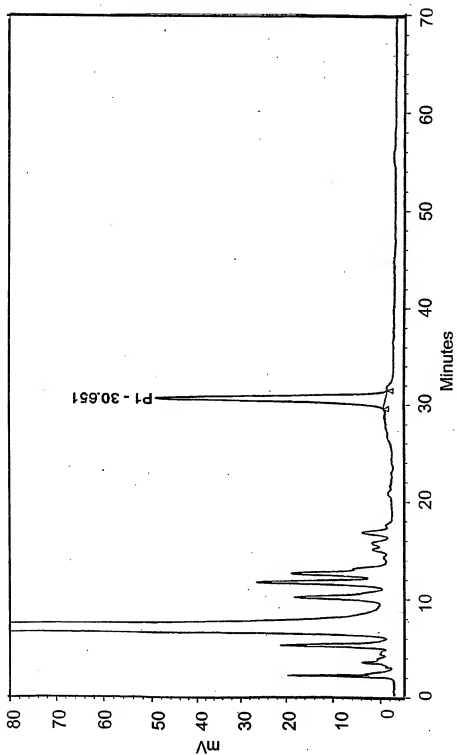


FIG. 124

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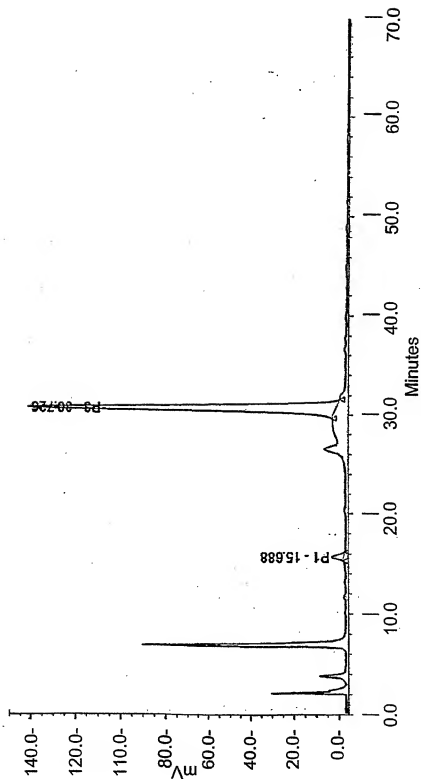


FIG. 125A

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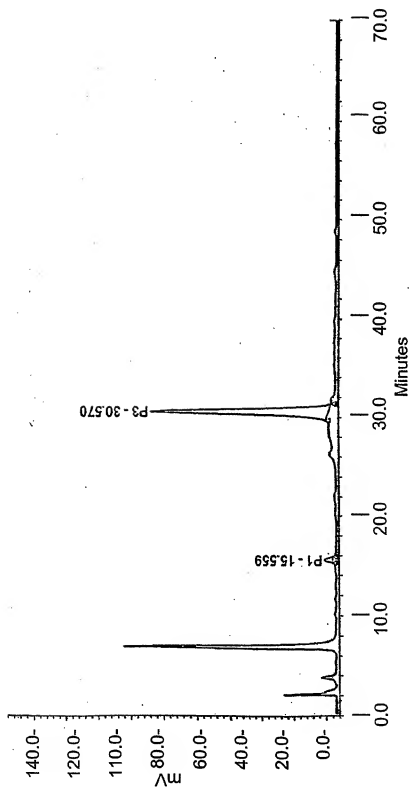


FIG. 125B

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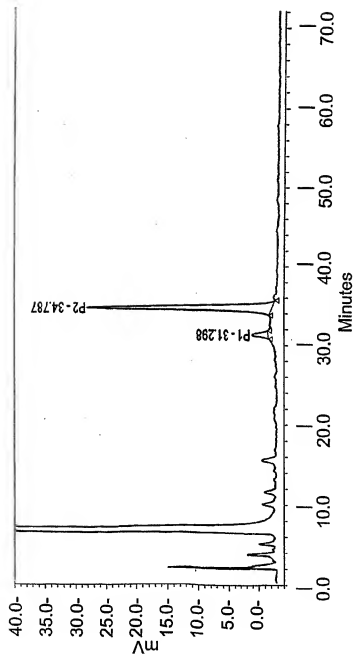


FIG. 126

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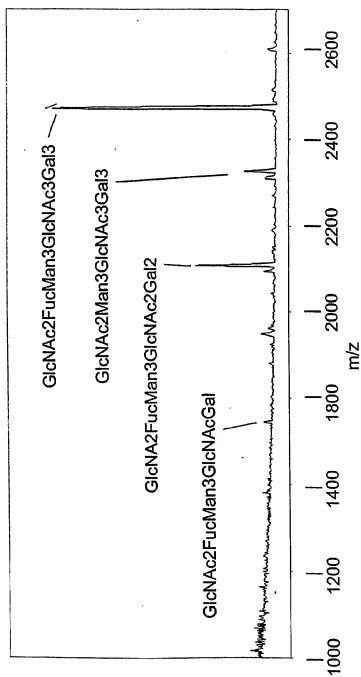


FIG. 127

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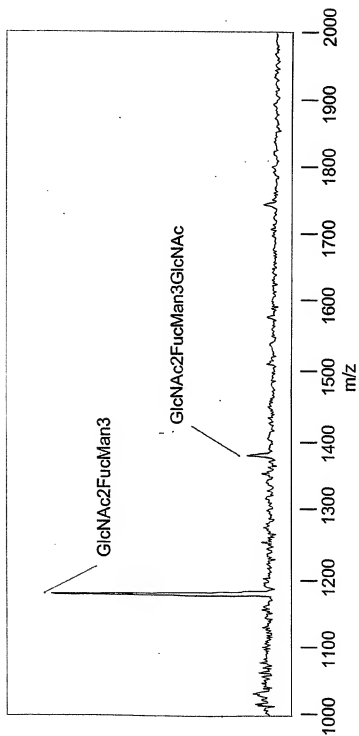


FIG. 128

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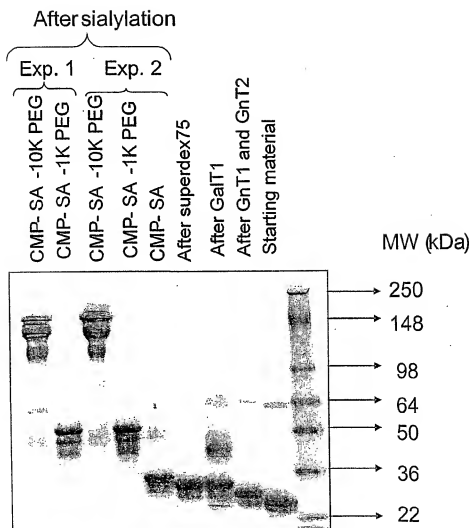


FIG. 129

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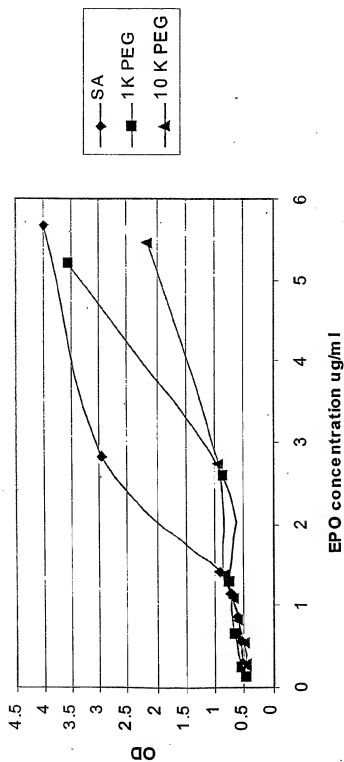
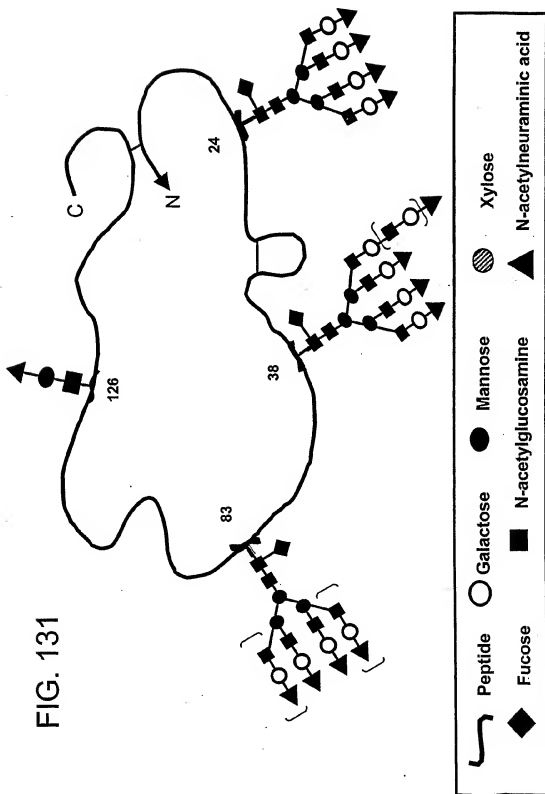


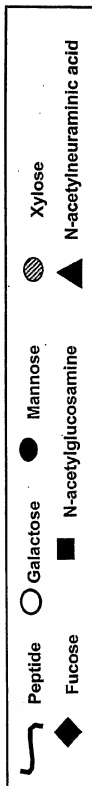
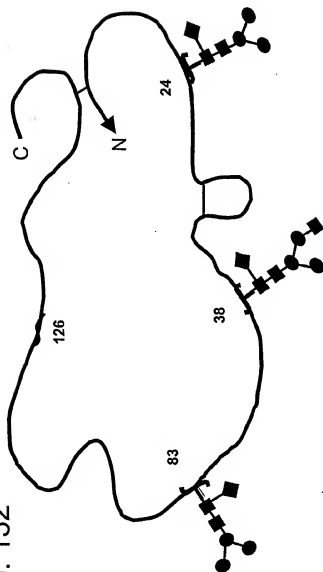
FIG. 130

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FIG. 132



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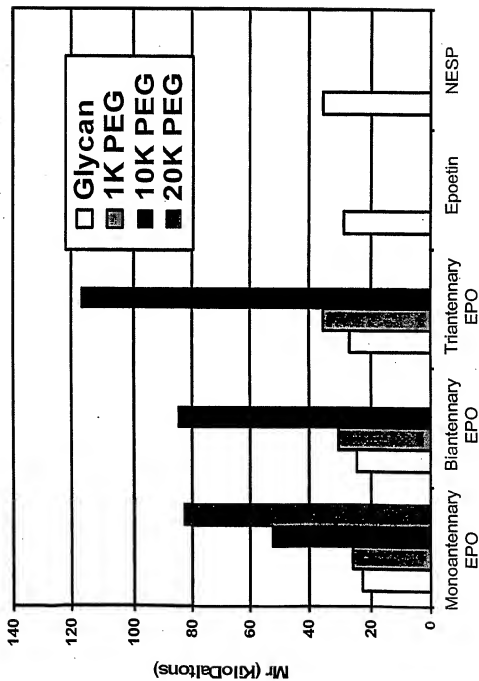


FIG. 133

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FIG. 134A

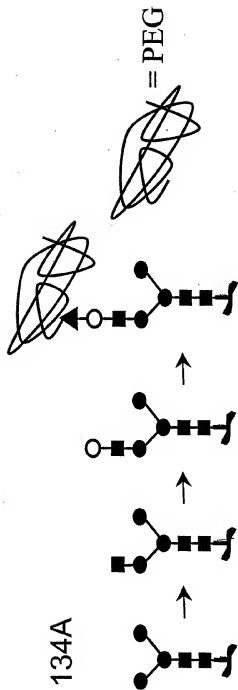
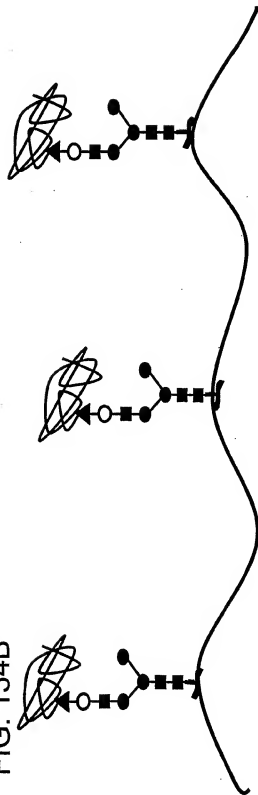


FIG. 134B



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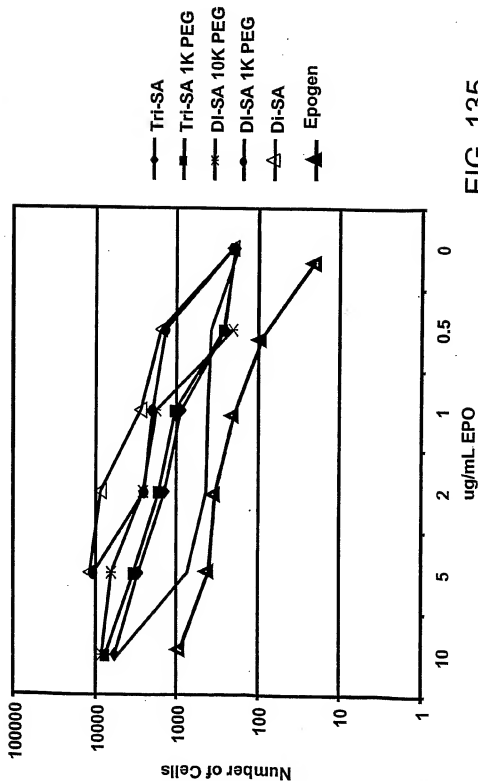


FIG. 135

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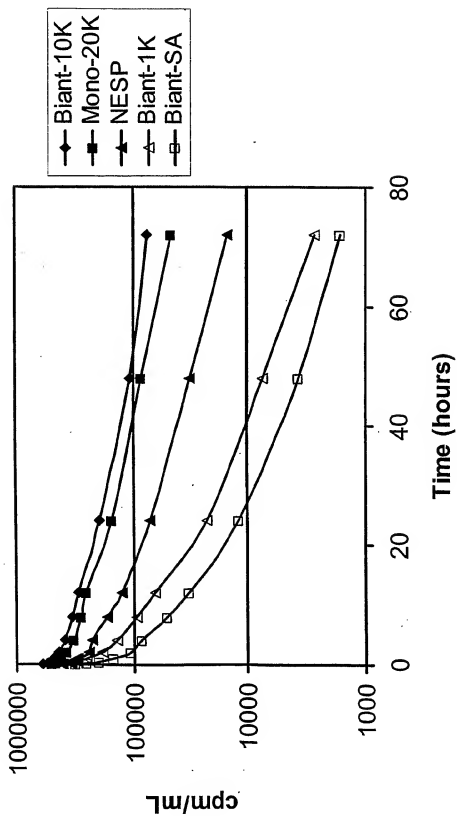


FIG. 136

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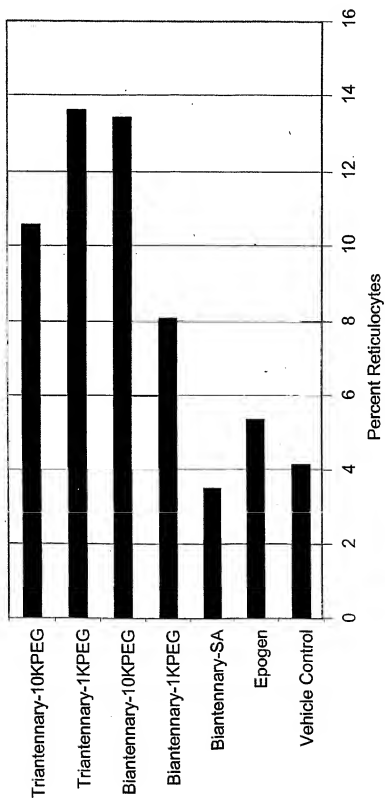


FIG. 137

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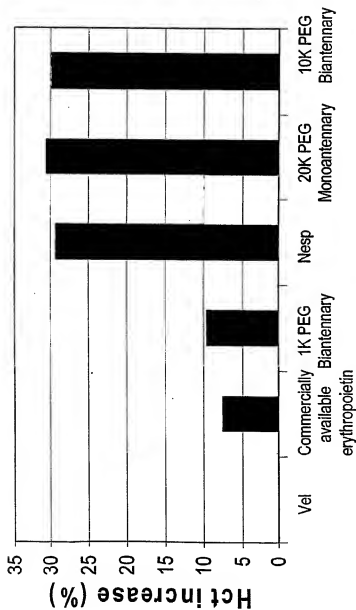


FIG. 138

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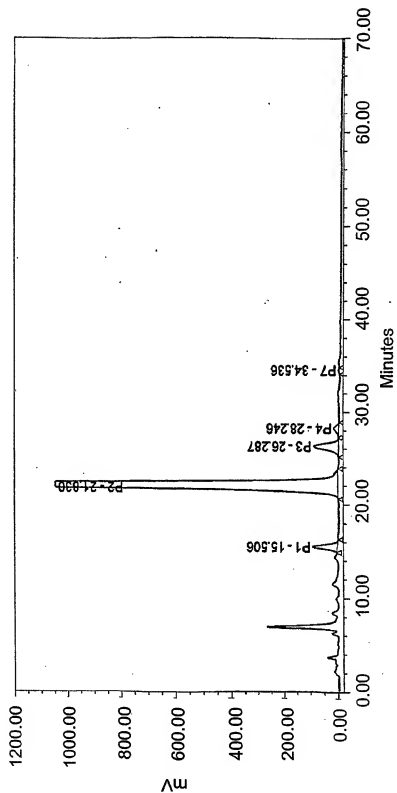


FIG. 139A

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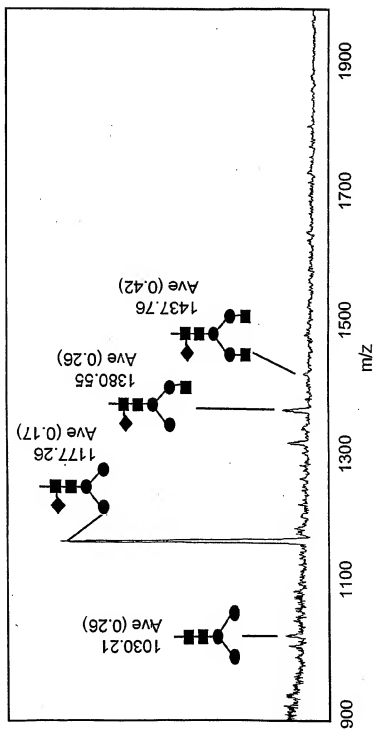


FIG. 139B

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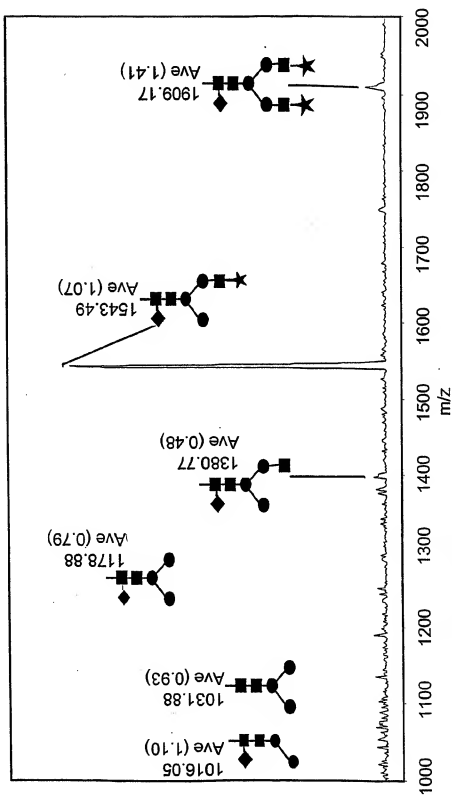


FIG. 140

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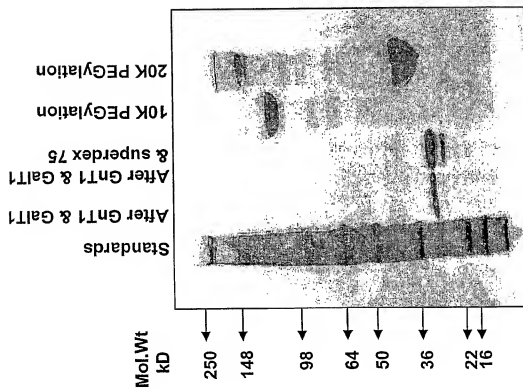


FIG. 141

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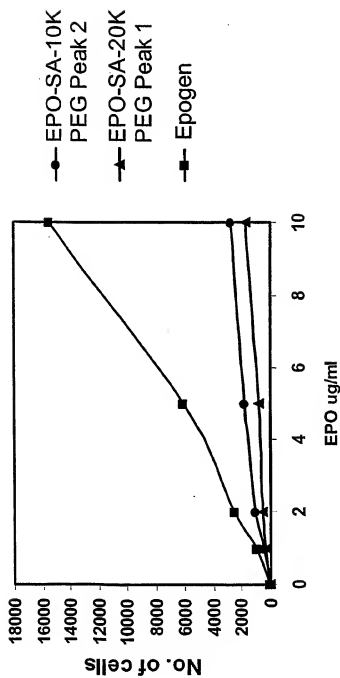


FIG. 142

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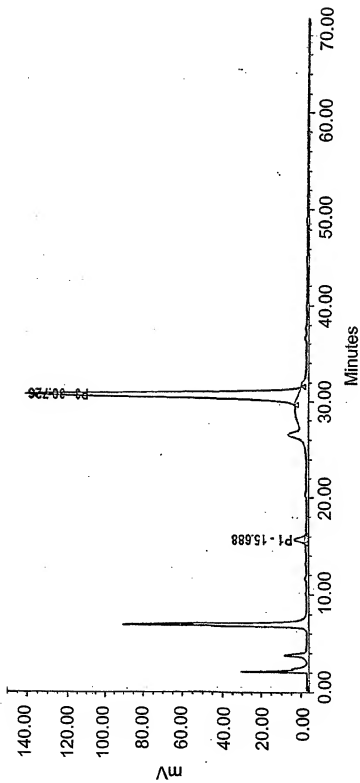


FIG. 143A

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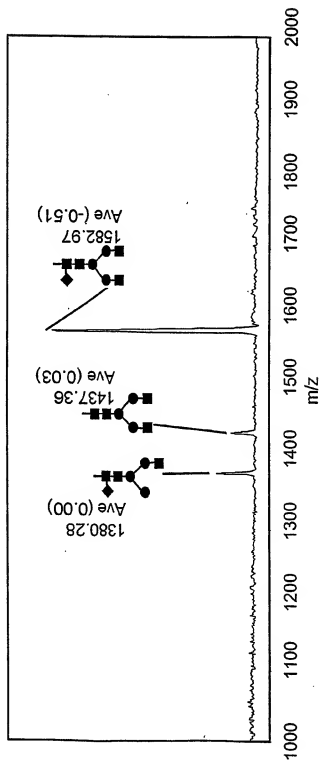


FIG. 143B

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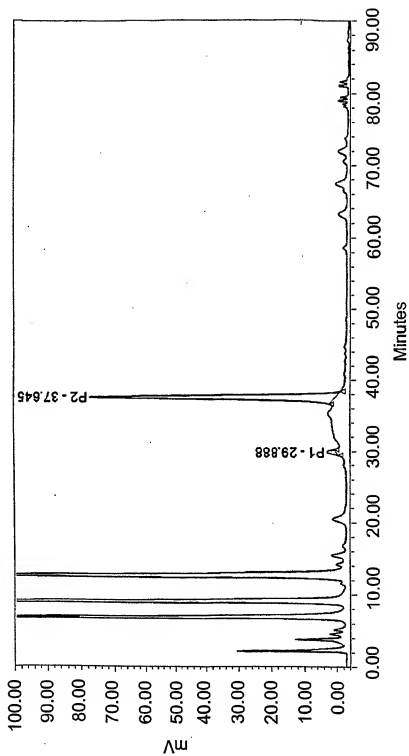


FIG. 144A

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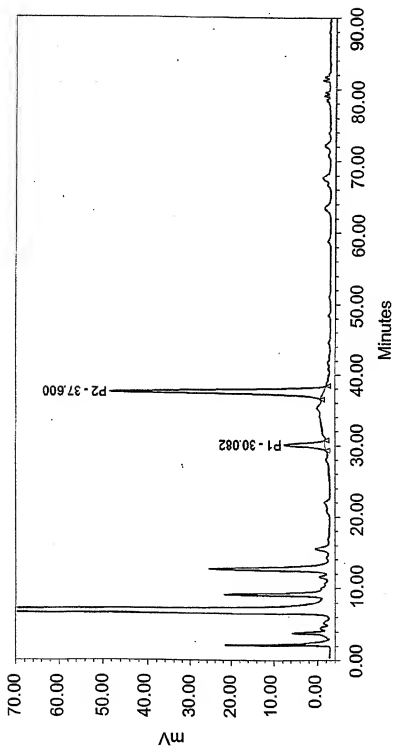


FIG. 144B

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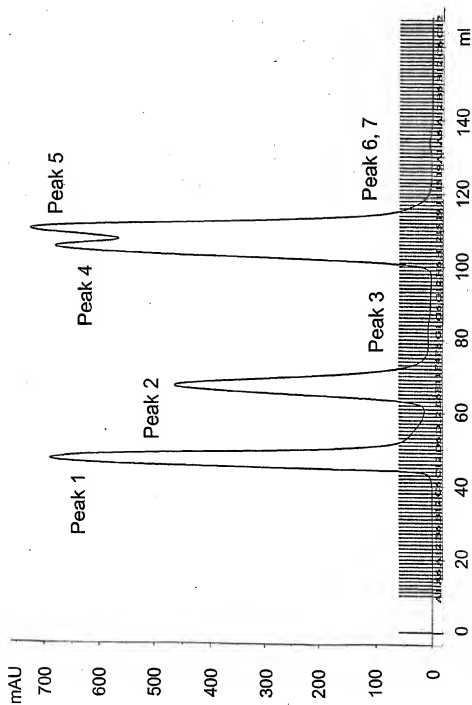


FIG. 145

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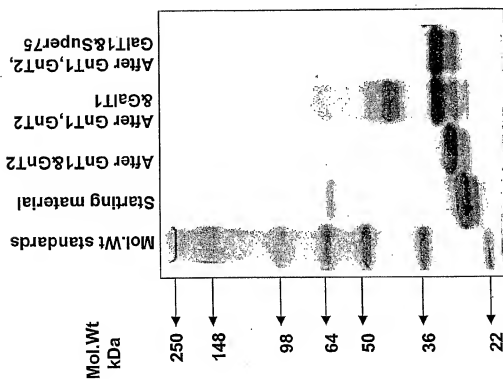


FIG. 146

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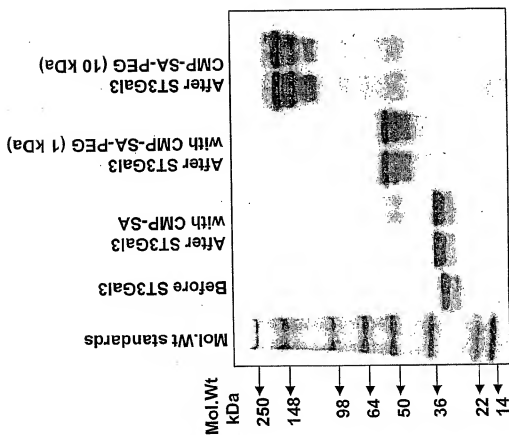


FIG. 147

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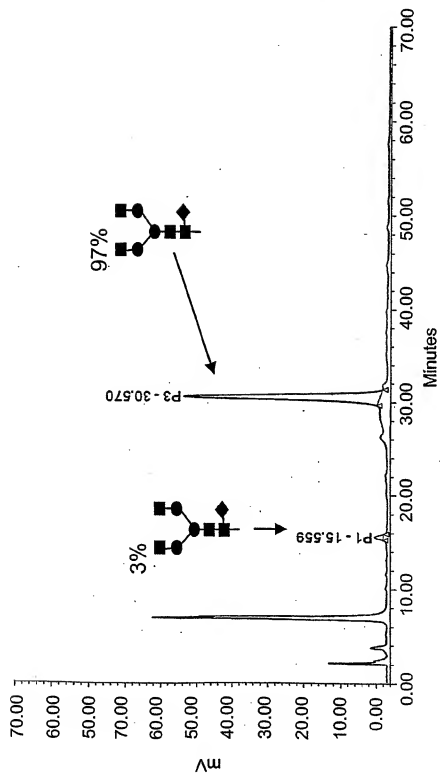


FIG. 148

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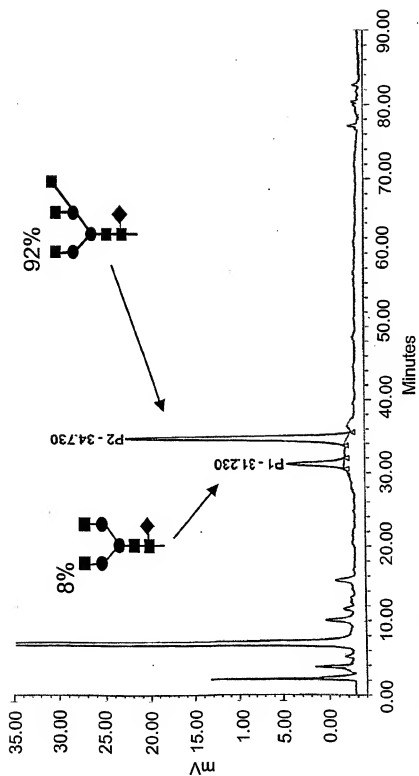


FIG. 149

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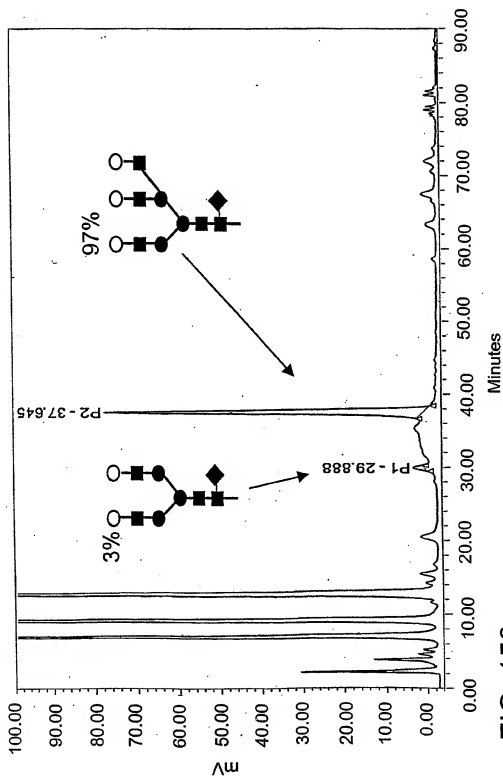


FIG. 150

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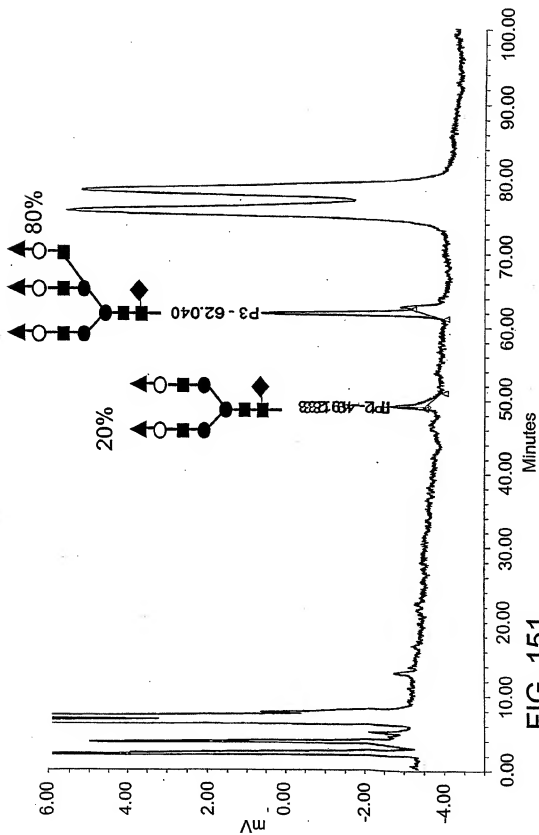


FIG. 151

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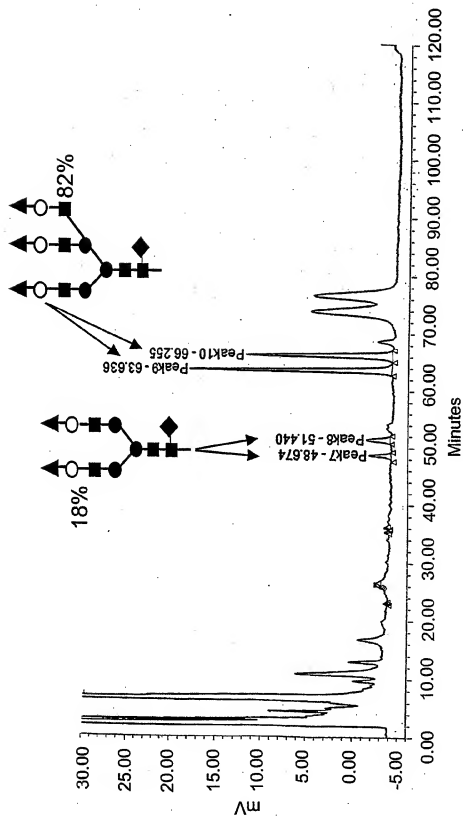


FIG. 152

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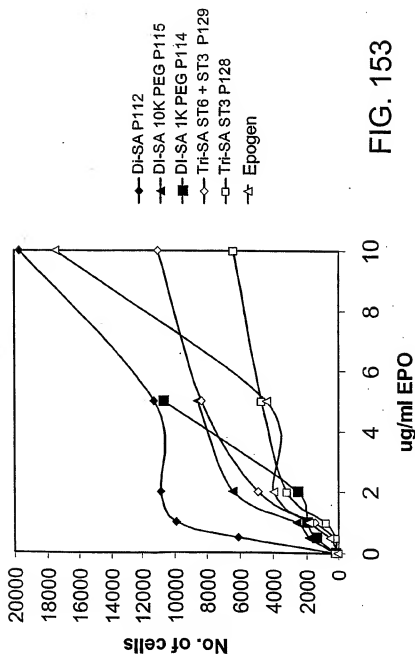


FIG. 153

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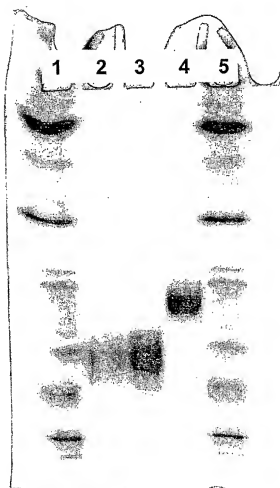


FIG. 154

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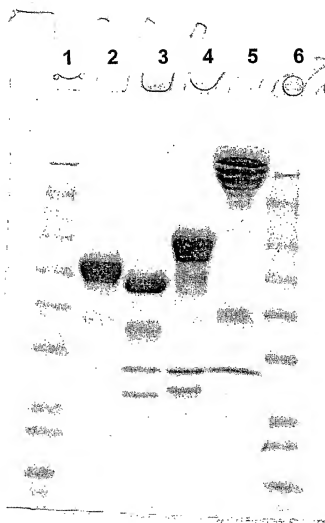


FIG. 155

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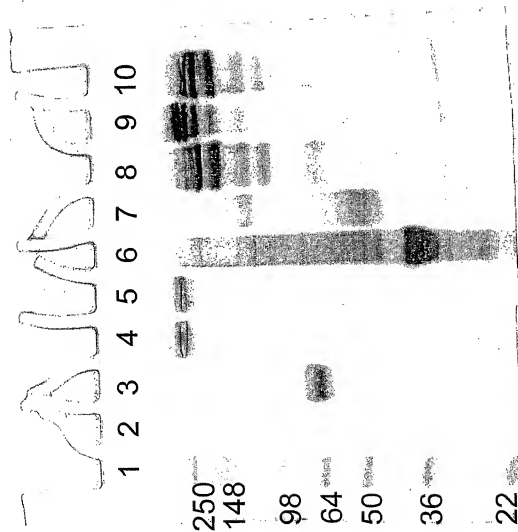


FIG. 156

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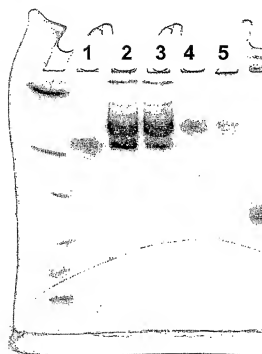


FIG. 157

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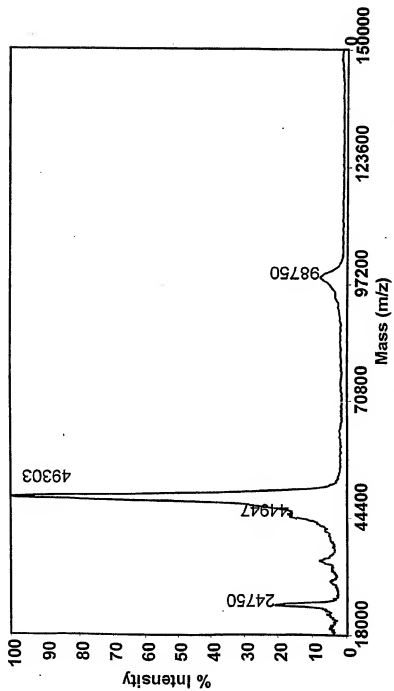


FIG. 158

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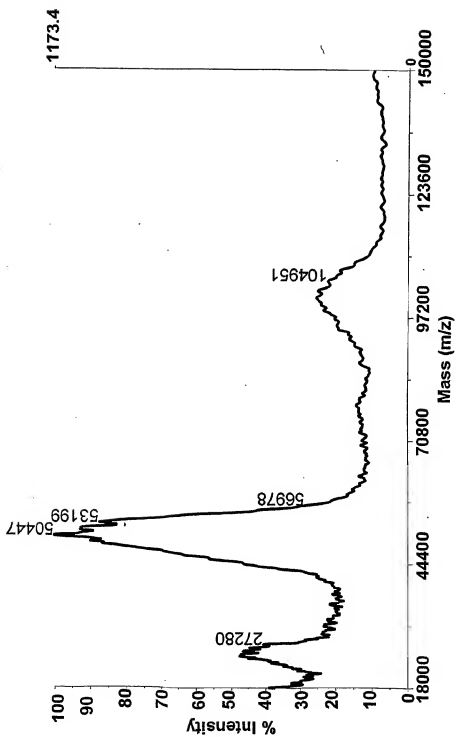


FIG. 159

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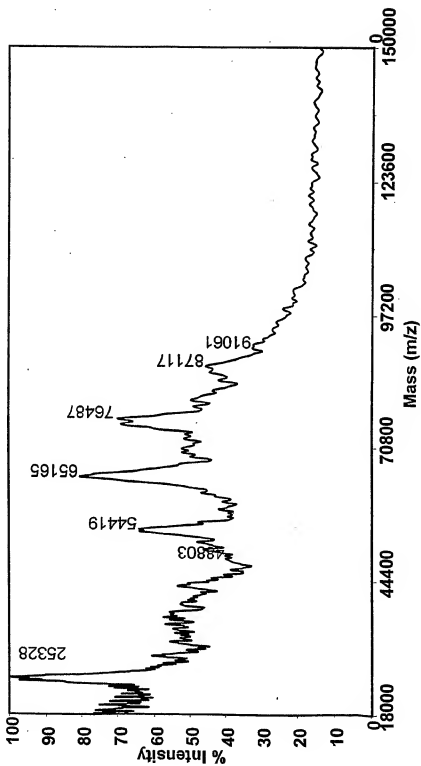


FIG. 160

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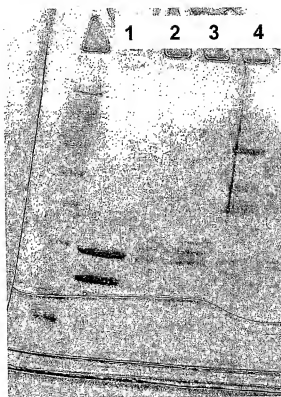


FIG. 161

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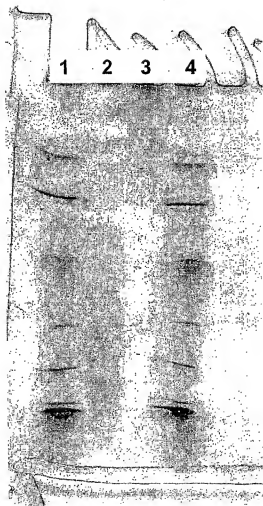


FIG. 162

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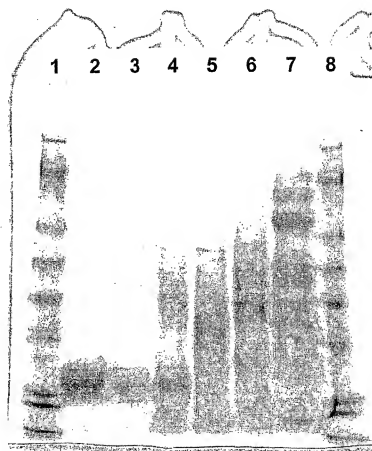


FIG. 163

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FIG. 164

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FIG. 165

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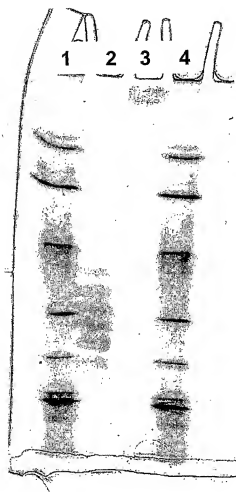


FIG. 166

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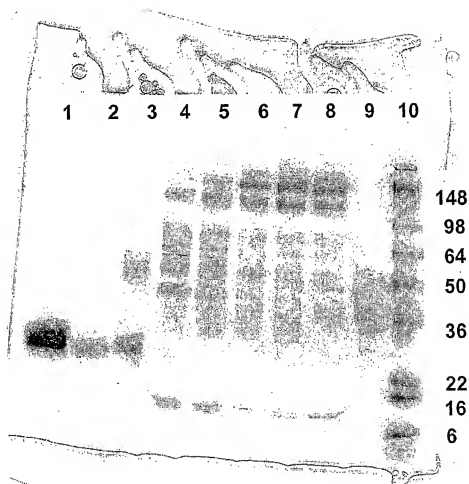


FIG. 167

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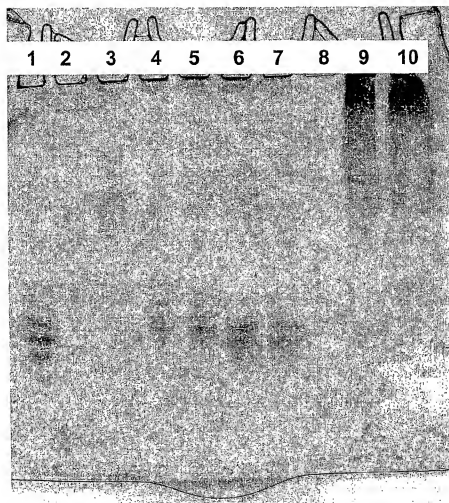
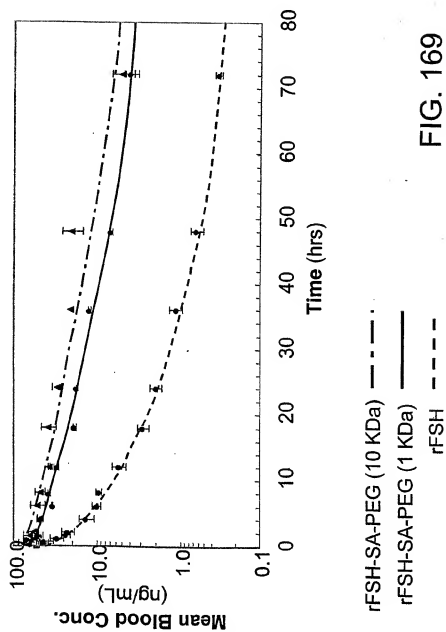


FIG. 168

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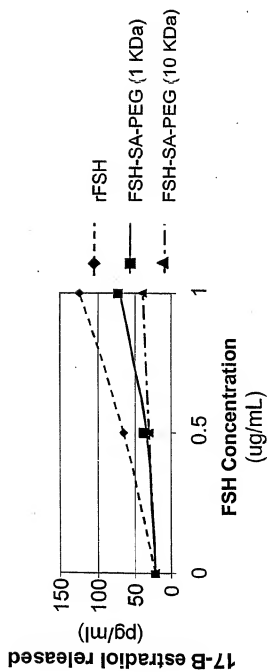


FIG. 170

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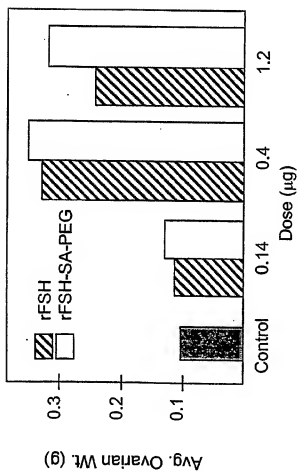


FIG. 171

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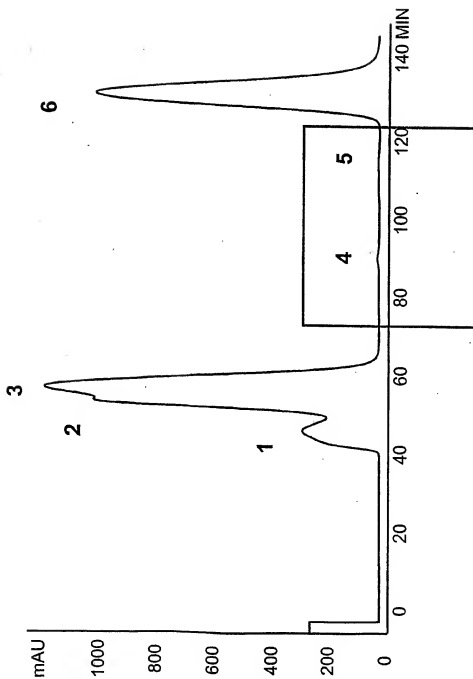


FIG. 172A

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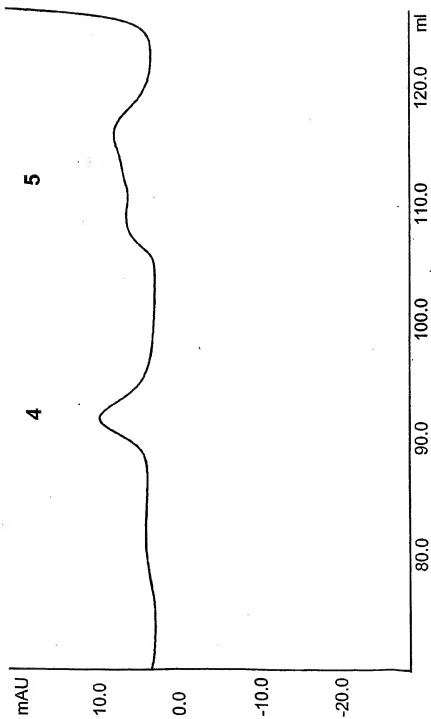


FIG. 172B

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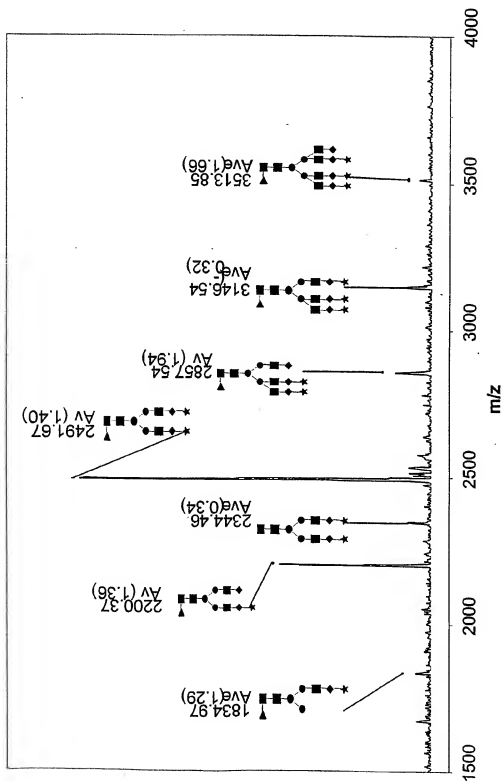


FIG. 173A

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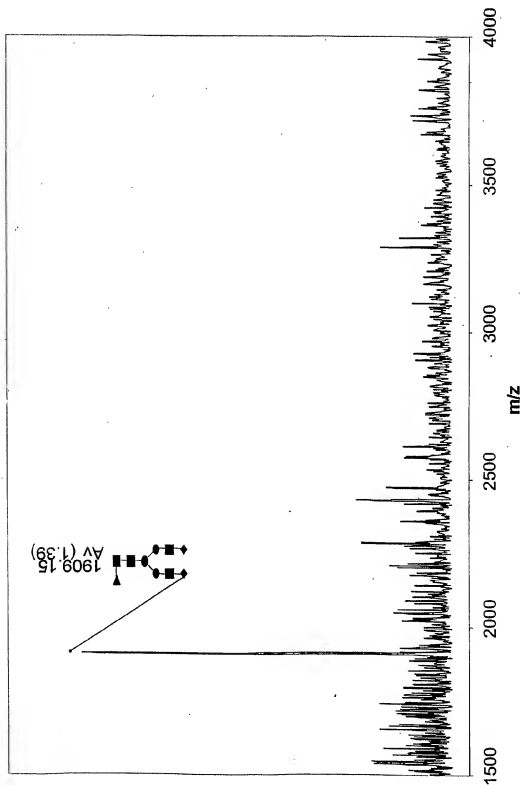


FIG. 173B

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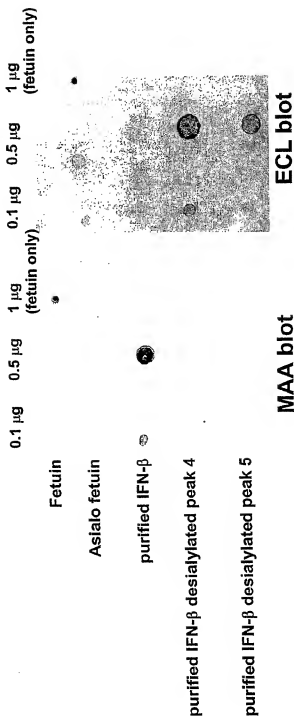


FIG. 174

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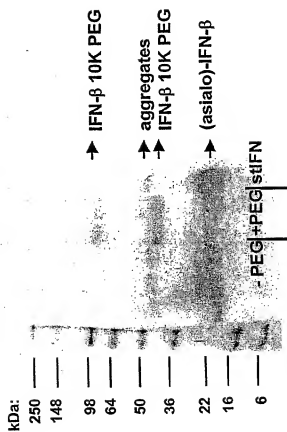
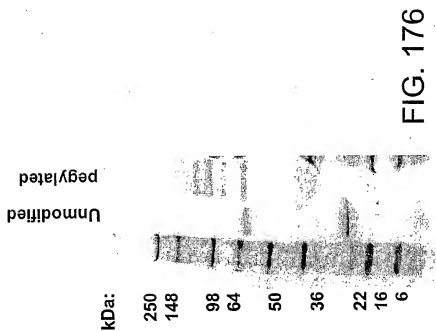


FIG. 175

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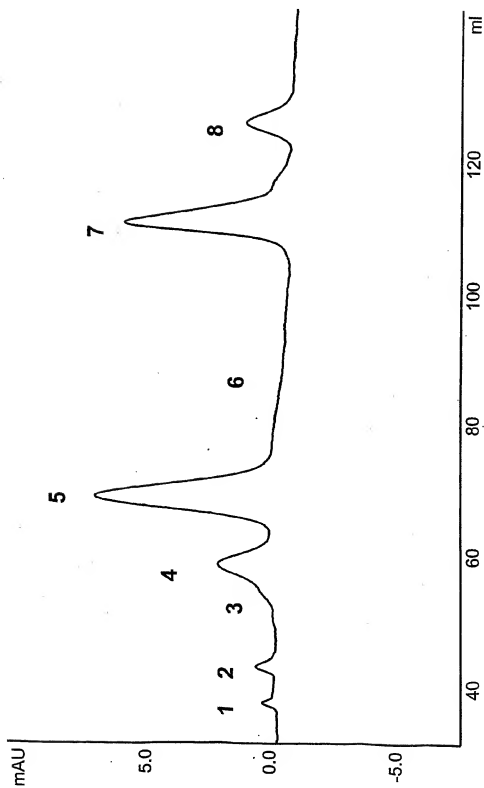


FIG. 177

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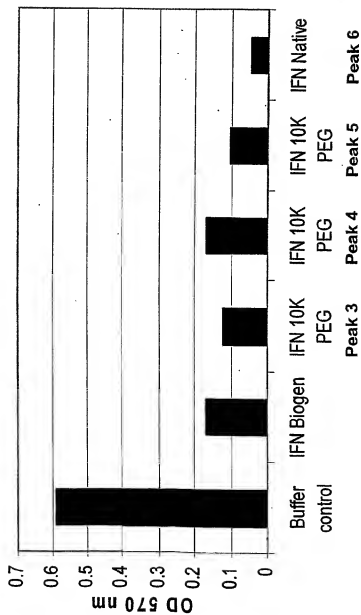


FIG. 178

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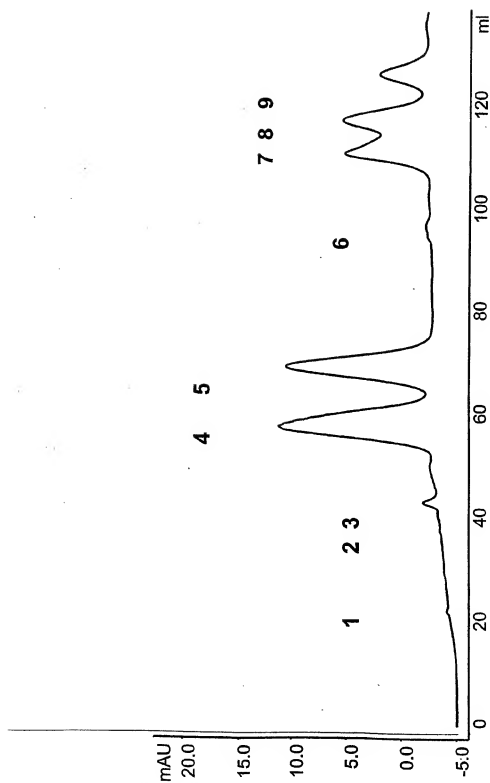


FIG. 179

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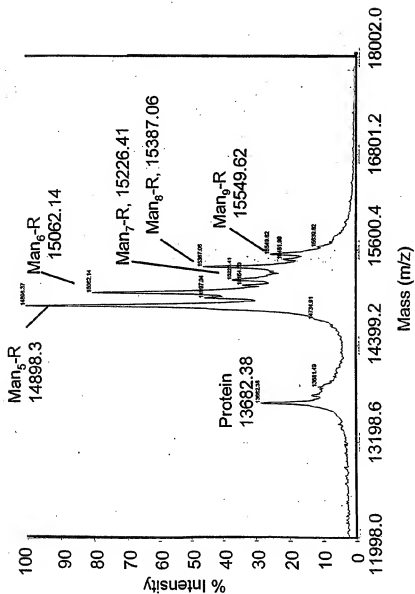


FIG. 180A

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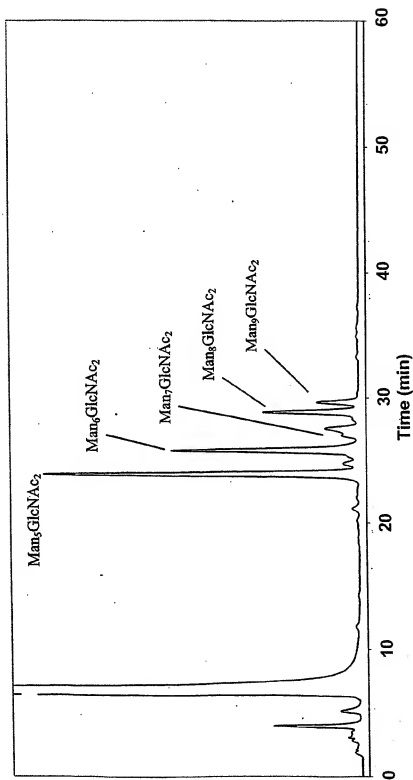


FIG. 180B

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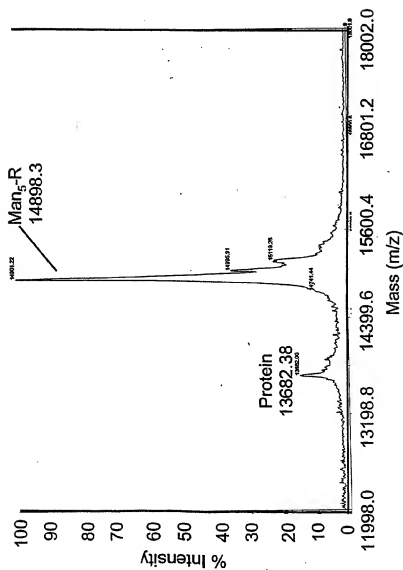


FIG. 182A

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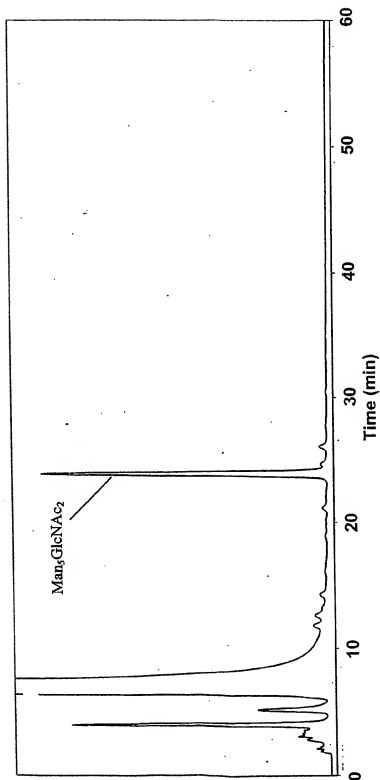


FIG. 182B

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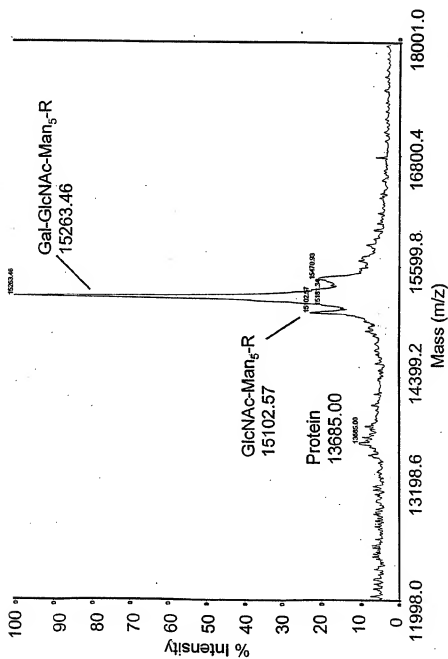


FIG. 185

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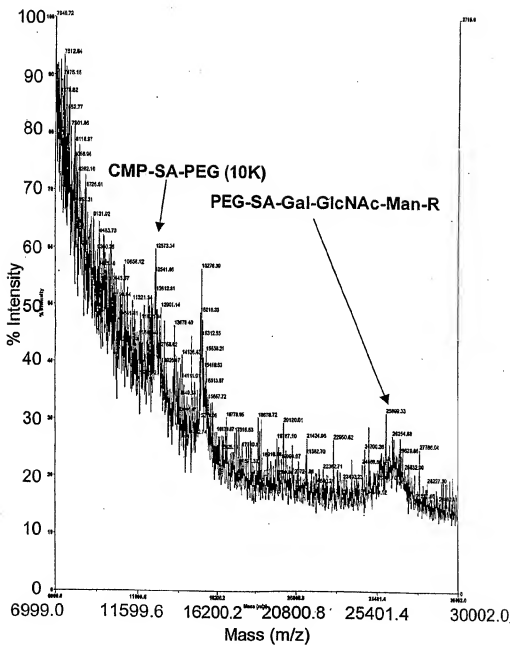
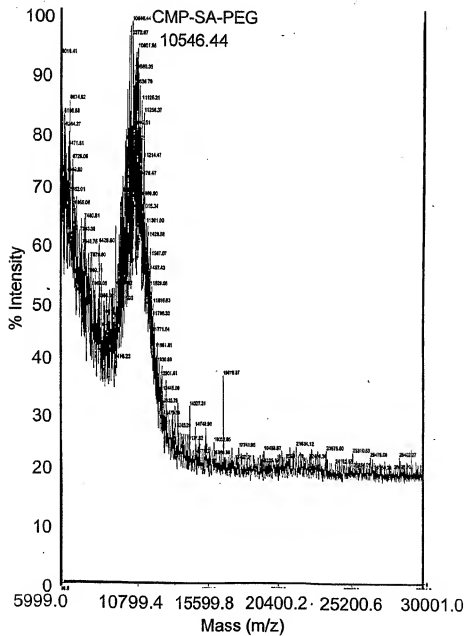


FIG. 187A

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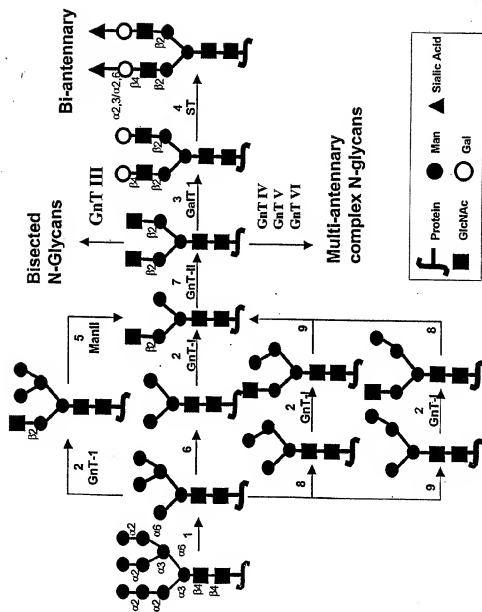


FIG. 188

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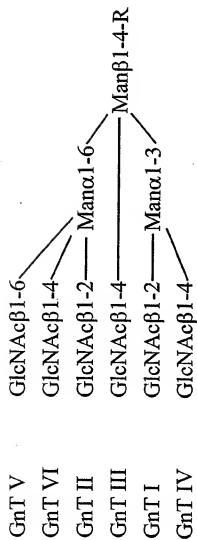


FIG. 189

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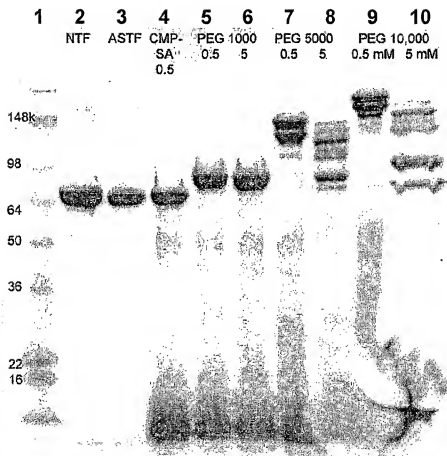


FIG. 190

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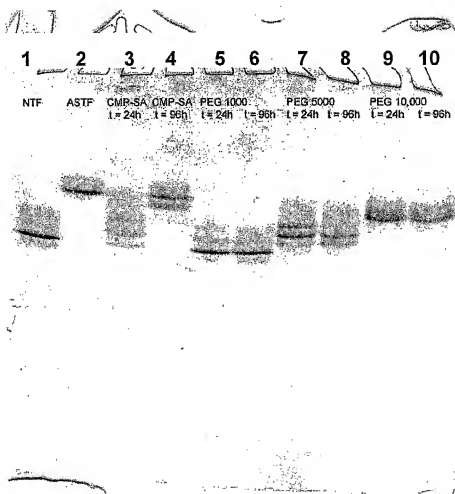
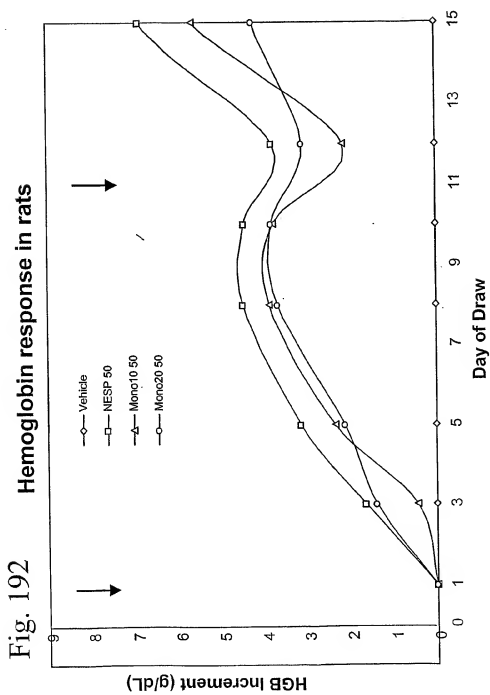


FIG. 191

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SEQUENCE LISTING

<110> Neose Technologies, Inc.
 DeFrees, Shawn
 Zopf, David
 Bayer, Robert
 Hakes, David
 Chen, Xi
 Bowe, Caryne

<120> ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF
 ERYTHROPOIETIN

<130> 040853-01-5083WO

<150> PCT/US02/32263
 <151> 2002-10-09

<150> US 10/287,994
 <151> 2002-11-5

<150> US 10/360,770
 <151> 2003-01-06

<150> US 10/369,779
 <151> 2003-03-17

<150> US 10/410,945
 <151> 2003-04-09

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 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Leu Val
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 165 170

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tcaagttaag taaaatgtca atagcctttt aatttaattt ttaattgttt tatcattcctt 120

tgcaataata aaacattaac ttatatacttt ttaattttaat gtatagaata gagatataca 180

taggatattgt aaatagatac acagtgtata tgtgattaaa atataatggg agattcaatc 240

agaaaaaagt ttctaaaaag gctctggggt aaaagaggaa ggaacaata atgaaaaaaa 300

tgtggtgaga aaacacagctg aaaccccatg taaagagtgt ataaagaaag caaaaagaga 360

agtgaagaat aacacagggg catttggaat atgtaaacga gtatgttccc tatttaaggc 420

taggcacaaa gcaaggtctt cagagaacct ggagcctaag gtttaggctc acccatttca 480

accagctctag cagcatctgc aacatctaca atggccttga cctttgcttt actggtggcc 540

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caaaaggctg aaaccatccc tgtctccatc gagatgatcc agcagatctt caatctcttc 780
agcacaaagg actcatctgc tgcctgggat gagaccctcc tagacaaatt ctacactgaa 840
ctctaccagc agctgaatga cctggaagcc tgtgtgatac aggggggtggg ggtgacagag 900
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aacaataata attctgctct cttgtgtatt tgatttttgt atgaaaaaaa ctaaaaatgg 1680
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20 25 30
Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
35 40 45
Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
50 55 60
Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65 70 75 80
Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser

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Ala	Ala	Trp	Asp	Glu	Thr	Leu	Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr				
			100						105					110					
Gln	Gln	Leu	Asn	Asp	Leu	Glu	Ala	Cys	Val	Ile	Gln	Gly	Val	Gly	Val				
			115					120					125						
Thr	Glu	Thr	Pro	Leu	Met	Lys	Glu	Asp	Ser	Ile	Leu	Ala	Val	Arg	Lys				
			130				135					140							
Tyr	Phe	Gln	Arg	Ile	Thr	Leu	Tyr	Leu	Lys	Glu	Lys	Lys	Tyr	Ser	Pro				
			145			150				155					160				
Cys	Ala	Trp	Glu	Val	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Leu				
				165					170						175				
Ser	Thr	Asn	Leu	Gln	Glu	Ser	Leu	Arg	Ser	Lys	Glu								
				180					185										

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 <213> Homo sapiens

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 ctctgtggc aattgaatgg gaggttgaa tattgctca aggacaggat gaactttgac 180
 atccttgagg agattaagca gctgcagcag ttccagaagg aggaagccgc attgaccatc 240
 tatgagatgc tccagaacat ctttgctatt ttcagacaag attcatctag cactggctgg 300
 aatgagacta ttgttgagaa cctctggct aatgtctatc atcagataaa ccacttgaag 360
 acagtctcgg aagaaaaact ggagaaagaa gattttacca ggggaaaact catgagcagt 420
 ctgcacctga aaagatatta tgggaggatt ctgcattacc tgaaggccaa ggagtacagt 480
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 cttacaggtt acotcogaaa ctgaagatct cctagcctgt cctctctggga ctggacaatt 600
 gcttoaagca ttctcaacc agcagatgct gtttaagtga ctgtaggcta atgtactgca 660
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Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30
 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45
 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60
 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80
 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95
 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110
 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125
 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140
 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160
 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
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 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 180 185

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<213> Homo sapiens

<400> 7

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 gcgttctctg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtg 180
 tccttcgagg aggcccgga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240
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 agtgaccaca cgggcaccaa gcgctcctgt cggtgccacg aggggtactc tctgtggca 480
 gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa 540
 aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaaggtgtg ccccaaaggg 600
 gagtgtccat ggcaggtcct gttgttggtg aatggagctc agttgtgtgg ggggaccctg 660

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atcaacacca tctgggtggt ctccggcgcc cactgtttcg acaaaatcaa gaactggagg 720
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cggcgggtgg cgcagggtcat catccccagc acgtacgtcc cgggcaccac caaccacgac 840
atcgcgctgc tccgcctgca ccagcccgtg gtectcactg accatgtggt gccctctgc 900
ctgcccgaa cggactgtct tgagaggagc ctggccttcg tgcgcttctc attggtcagc 960
ggctggggcc agctgctgga cctggcgcc acggcccttg agctcatggt gctcaacgtg 1020
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atcacggagt acatgttctg tgcgggtac tcggatggca gcaaggactc ctgcaagggg 1140
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agctggggcc agggctgcgc aacctgggc cactttgggg tgtacaccag ggtctccag 1260
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<211> 444
<212> PRT
<213> Homo sapiens

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20 25 30
Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
35 40 45
Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
50 55 60
Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65 70 75 80
Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
85 90 95
Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
100 105 110
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
115 120 125
Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
130 135 140
Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145 150 155 160
Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
165 170 175

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Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190
 Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205
 Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
 210 215 220
 Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
 225 230 235 240
 Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255
 Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270
 Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285
 Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300
 Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320
 Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335
 Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350
 Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365
 Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380
 Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400
 Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415
 Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
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 Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
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<211> 1437

<212> DNA

<213> Homo sapiens

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ctgaatcggc caaagaggt taattcaggt aaattggaag agtttgttca agggaaacctt 180
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 tttaatgact tcactcgggt tgttgggtgga gaagatgcca aaccaggcca attcctttgg 720
 caggttgttt tgaattgtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa 780
 tggattgtaa ctgtgtccca ctgtgttgaa actggtgtta aaattacagt tgtcgcagggt 840
 gaacataata ttgaggagac agaacataca gagcaaaagc gaaatgtgat tcgagcaatt 900
 attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccttctg 960
 gaactggagc aaoccttagt gctaaacagc tacgttacac ctatttgcatt tgctgacaag 1020
 gaatacacga acatcttctt caaatttgga tctggctatg taagtggctg ggcaagagtc 1080
 ttccacaaag ggagatcagc tttagttctt cagtacctta gagttccact tgttgaccga 1140
 gccacatgtc ttgatctac aaagtccacc atctataaca acatgttctg tgctggcttc 1200
 catgaaggag gtgagagatc atgtcaaggga gatagtggg gacccatgt tactgaagtg 1260
 gaagggacca gtttcttaac tggaattatt agctggggtg aagagtgtgc aatgaaaggc 1320
 aaatattgaa tatataccaa ggtatccogg tatgtcaact ggattaagga aaaaaccaag 1380
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<210> 10
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 10
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 1 5 10 15
 Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
 20 25 30
 Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
 35 40 45
 Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys

50	55	60
Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn		
65	70	75 80
Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln		
	85	90 95
Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile		
	100	105 110
Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys		
	115	120 125
Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe		
	130	135 140
Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly		
	145	150 155 160
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe		
	165	170 175
Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala		
	180	185 190
Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu		
	195	200 205
Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe		
	210	215 220
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp		
	225	230 235 240
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile		
	245	250 255
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly		
	260	265 270
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu		
	275	280 285
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His		
	290	295 300
Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu		
	305	310 315 320
Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys		
	325	330 335
Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly		
	340	345 350
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu		
	355	360 365
Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu		
	370	375 380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
450 455 460

<210> 11
<211> 603
<212> DNA
<213> Homo sapiens

<400> 11
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ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca 180
tatccactc cactaagtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240
tcacattgct gtgtagctaa atcatataac agggtcacag taatgggggg tttaaagtgt 300
gagaaccaca cggcgtgcc ctgcagtact tgttattatc acaaatotta aatgttttac 360
caagtgcgtt ctgtgatgact gctgattttc tggaatggaa aattaagttg ttagtggttt 420
atggccttgt gagataaaac tctccttttc ctaccatac cactttgaca cgcttcaagg 480
atatactgca gcttactgc ctctctcctt atctacagc acaatcagca gctagttct 540
tttcatttgg aatgaataca gcattaagct tgttccactg caaataaagc cttttaaatc 600
atc 603

<210> 12
<211> 116
<212> PRT
<213> Homo sapiens

<400> 12
Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1 5 10
Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
20 25 30
Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
35 40 45
Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
85 90 95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
100 105 110

Tyr His Lys Ser
115

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13
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tgtgagctga ccaacatcac cattgcaata gagaagaag aatgtcggtt ctgcataagc 120
atcaacacca ctgtggtgctc tggctactgc tacaccaggg atctggtgta taaggaccca 180
gccaggccca aaatccagaa aacatgtacc ttcaaggaa tggtatatga aacagtgaga 240
gtgcccgct gtgctcacca tgcagattcc ttgtatacat acccagtgcc caccagtggt 300
cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggccacagc 360
tactgctcct ttggtgaat gaaagaataa 390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14
Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys

115

120

125

Glu

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<210> 15
<211> 1342
<212> DNA
<213> Homo sapiens

<400> 15
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ccgccctctc ctccaggccc gtggggctgg cctgcacccg ccgagcttcc cgggatgagg 120
gcccccggtg tggtcacccg gcgcgcacca ggtcgctgag ggaccccggc caggcgcgga 180
gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc 240
tctgggcctc ccagtctcgg gcgccccacc acgcctcacc tgtgacagcc gagtccctgga 300
gaggtagctc ttggaggcca aggaggccga gaatatcacg acgggctgtg ctgaacactg 360
cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag 420
gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc 480
tgtcctgcgg ggcacaggccc tgttggtcaa ctcttcccag ccgtgggagc cctgcagct 540
gcatgtggat aaagccgtca gtggccttcg cagcctcacc actctgcttc gggctctgcg 600
agcccagaag gaagccatct cccctccaga tgcggcctca gctgctccac tccgaacaat 660
cactgctgac actttccgca aactcttccg agtctaactc aatttctcc ggggaaagct 720
gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccaggtg tgtccacctg 780
ggcatatcca ccacctccct caccaacatt gcttgtgcca caccctcccc gcgcactcct 840
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gcaatgacat ctacggggcc agagggaactg tccagagagc aactctgaga tctaaggatg 960
tcacagggcc aacttgaggg ccagagcagc gaagcattca gagagcagct ttaactoaag 1020
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ggtggcaaga gcccccctga cacgggggtg gtgggaacca tgaagacagg atgggggctg 1260
gcctctggct ctcatggggt ccaagttttg tgtattcttc aaactcattg acaagaactg 1320
aaaccaccaa aaaaaaaaaa aa 1342

<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

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<400> 16

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Arg

<210> 17

<211> 435

<212> DNA

<213> Homo sapiens

<400> 17

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 cgtctctga acctgagtag agacactgct gctgagatga atgaacacagt agaagtcac 180
 tcagaaatgt ttgacctoca ggagccgacc tgcctacaga cccgcttgga gctgtacaag 240
 cagggcctgc ggggcagcct caccagctc aagggccct tgaccatgat gccagccac 300
 tacaagcagc actgccctcc aaccccgaa acttctgtg caaccagat taccacctt 360
 gaaagtcca aaggaacct gaaggacttt ctgcttgtca tcccctttga ctgctgggag 420

ccagtcagg agtga

435

<210> 18
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
 1 5 10 15
 Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
 20 25 30
 Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
 35 40 45
 Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
 50 55 60
 Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
 65 70 75 80
 Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
 85 90 95
 Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
 100 105 110
 Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
 115 120 125
 Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 130 135 140

<210> 19
 <211> 501
 <212> DNA
 <213> Homo sapiens

<400> 19
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 tgttactgcc aggaccata tgtaaaagaa gcagaaaacc ttaagaataa ttttaatgca 120
 ggctattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180
 gaggagagtg acagaaaaat aatgcagagc caaattgtct ccttttactt caaacttttt 240
 aaaaacttta aagatgacca gagcatocaa aagagtgtgg agaccatcaa ggaagacatg 300
 aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360
 tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420
 gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480
 ggctgaagag catcccagta a 501
 <210> 20
 <211> 166

<212> PRT

<213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
20 25 30Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
35 40 45Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
50 55 60Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65 70 75 80Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
85 90 95Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
100 105 110Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
115 120 125Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
130 135 140Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145 150 155 160Gly Arg Arg Ala Ser Gln
165

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

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cctgtgtctgc ctggtccctg tctccctggc tgaggatccc caggagatg ctgccacaga 120

gacagatata tcccaccatg atcaggatca cccaaccttc aacaagatca cccccaacct 180

ggctgagttc gccttcagcc tataccgaca gctggcacac cagtccaaca gcaccaatat 240

cttctctctc ccagtgagca togctacagc ctttgcaatg ctctccctgg ggaccaaggc 300

tgacaactca gatgaaatcc tggaggggcct gaattcaac ctacaggaga ttccggaggc 360

tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct 420

ccagctgacc acocggcaatg gcctgttcct cagcgagggc ctgaagctag tggataagtt 480

tttgagggat gttaaaaagt tgtaccacto agaagccttc actgtcaact tcggggacac 540

cgaagaggcc aagaacacaga tcaacgatta cgtggagaag ggtactcaag ggaaatgtgt 600
 ggatttggtc aaggagcttg acagagacac agtttttctg ctggtgaatt acatcttctt 660
 taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt 720
 ggaccagggtg accaccgtga aggtgcctat gatgaagcgt ttaggcatgt ttaacatcca 780
 gcaactgaag aagctgtcca gctgggtgct gctgatgaaa tacctgggca atgccaccgc 840
 catcttcttc ctgcctgatg aggggaaact acagcacctg gaaaatgaac tcacccacga 900
 tatcatcacc aagttcctgg aaaatgaaga cagaaggtct gccagcttac atttaccxaa 960
 actgtocatt actggaacct atgatctgaa gagcgtcctg ggccaactgg gcatacctaa 1020
 ggtcttcagc aatggggctg acctctccgg ggtcacagag gaggcacccc tgaagctctc 1080
 caaggccgtg cataaggctg tgctgacctat cgacgagaaa gggactgaag ctgctggggc 1140
 catgttttta gagggccatac ccattgtctat ccccccgag gtcaagtcca acaaacctt 1200
 tgtctcttta atgattgaac aaaataccaa gtctccctc ttcatgggaa aagtgggtgaa 1260
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 cctggatga cattaagaa gggttgagct gg 1352

<210> 22
 <211> 418
 <212> PRT
 <213> Homo sapiens

<400> 22
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 1 5 10 15
 Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
 20 25 30
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 35 40 45
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 50 55 60
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 65 70 75 80
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 85 90 95
 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
 100 105 110
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 115 120 125
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 145 150 155 160
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 165 170 175
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 180 185 190
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 195 200 205
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 210 215 220
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
 225 230 235 240
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 245 250 255
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 260 265 270
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 275 280 285
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415
 Gln Lys
 <210> 23
 <211> 2004
 <212> DNA
 <213> Homo sapiens
 <400> 23
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ctctatcctt cagagactct ggaacccttg tggctctctc ttcattctaat gacctgaggg 120
 ggatggagtt ttcaagtctt tcacagagagg aatgtcccaa gcctttgagt agggtaagca 180
 tcatggcttg cagcctcaca ggtttgcttc tacttcaggc agtgctctgg gcatcaggtg 240
 cccgcccctg catccctaaa agcttcggct acagctcggg ggtgtgtgtc tgcattgcca 300
 catactgtga ctcccttgac ccccgacct ttcttgccct tggtaacctc agccgctatg 360
 agagtacacg cagtgggcga cggatggagc tgagtatggg gcccatccag gctaatacaca 420
 cgggcacagg cctgctactg aacctgcagc cagaacagaa gttccagaaa gtgaagggat 480
 ttggaggggc catgacagat gctgctgtct tcaacatcct tgccctgtca cccctgtccc 540
 aaaatttgct acttaaatcg tacttctctg aagaaggaat cggatataac atcatccggg 600
 taoccatggc cagctgtgac ttctccatcc gcacctacac ctatgcagac acccctgatg 660
 atttccagtt gcacaacttc agcctcccag aggaagatag caagctcaag atacctctga 720
 ttacccagc cctgcagttg gccagcgtc ccgtttcact ccttgccagc ccctggacat 780
 caoccatctg gctcaagacc aatggagcgg tgaatgggaa ggggtcactc aaggacagc 840
 ccggagacat ctaccaccag aacctgggca gatactttgt gaagtctctg gatgcctatg 900
 ctgagcaciaa gttacagttc tgggcagtg cagctgaaaa tgagccttct gctgggctgt 960
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 ccgtgacct aggtcctacc ctogccaaca gtactcaaca caatgtccgc ctactcatgc 1080
 tggatgacca acgcttgctg ctgcccact gggcaaaagt ggtactgaca gaccagaag 1140
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 ggggcaatgg tttgggtgac tcaatttccc ctctaggtgg tgccaggggc tggaggcccc 1920

tagaaaaaga tcagtaagcc ccagtgcccc ccagccccc atgettattgt gaacatgcgc 1980
 tgtgtgctgc ttgctttgga aact 2004

<210> 24
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
 1 5 10 15
 Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Gln
 20 25 30
 Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45
 Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60
 Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
 65 70 75 80
 Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95
 Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110
 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125
 Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140
 Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160
 Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175
 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190
 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205
 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
 210 215 220
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 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
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 Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
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 Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
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 Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
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 His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
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 Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
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 Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
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 Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270
 Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
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 Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
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 Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
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 Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
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 Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
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 Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
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 Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
 370 375 380
 Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 385 390 395 400
 Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
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 Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
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 Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
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 Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
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 His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys

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Gly Val Lys His Leu Lys Asp Phe	Pro Ile Leu Pro Gly Glu Ile Phe																												
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Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly	Pro Thr Lys Ser Asp																												
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Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg																													
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Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val																													
580	585																												
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610	615																												
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val																													
625	630																												
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Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp																													
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Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg																													
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Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp																													
770	775																												
Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys																													
785	790																												
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Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr																													
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Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
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 850 855 860
 Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
 865 870 875 880
 Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
 885 890 895
 Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
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 Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Ser Ser Met
 915 920 925
 Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
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 Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
 945 950 955 960
 Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
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 Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
 980 985 990
 Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
 995 1000 1005
 Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser
 1010 1015 1020
 Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser
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 Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu
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 Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg
 1055 1060 1065
 Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met
 1070 1075 1080
 Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln
 1085 1090 1095
 Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met
 1100 1105 1110
 Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile
 1115 1120 1125
 Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro
 1130 1135 1140

Ser Pro	Lys Gln	Leu Val	Ser	Leu Gly	Pro Glu	Lys	Ser Val	Glu
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Gly Gln	Asn Phe	Leu Ser	Glu	Lys Asn	Lys Val	Val	Val Gly	Lys
1160			1165			1170		
Gly Glu	Phe Thr	Lys Asp	Val	Gly Leu	Lys Glu	Met	Val Phe	Pro
1175			1180			1185		
Ser Ser	Arg Asn	Leu Phe	Leu	Thr Asn	Leu Asp	Asn	Leu His	Glu
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Asn Asn	Thr His	Asn Gln	Glu	Lys Lys	Ile Gln	Glu	Glu Ile	Glu
1205			1210			1215		
Lys Lys	Glu Thr	Leu Ile	Gln	Glu Asn	Val Val	Leu	Pro Gln	Ile
1220			1225			1230		
His Thr	Val Thr	Gly Thr	Lys	Asn Phe	Met Lys	Asn	Leu Phe	Leu
1235			1240			1245		
Leu Ser	Thr Arg	Gln Asn	Val	Glu Gly	Ser Tyr	Asp	Gly Ala	Tyr
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Ala Pro	Val Leu	Gln Asp	Phe	Arg Ser	Leu Asn	Asp	Ser Thr	Asn
1265			1270			1275		
Arg Thr	Lys Lys	His Thr	Ala	His Phe	Ser Lys	Lys	Gly Glu	Glu
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Glu Asn	Leu Glu	Gly Leu	Gly	Asn Gln	Thr Lys	Gln	Ile Val	Glu
1295			1300			1305		
Lys Tyr	Ala Cys	Thr Thr	Arg	Ile Ser	Pro Asn	Thr	Ser Gln	Gln
1310			1315			1320		
Asn Phe	Val Thr	Gln Arg	Ser	Lys Arg	Ala Leu	Lys	Gln Phe	Arg
1325			1330			1335		
Leu Pro	Leu Glu	Glu Thr	Glu	Leu Glu	Lys Arg	Ile	Ile Val	Asp
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Ser Thr	Leu Thr	Gln Ile	Asp	Tyr Asn	Glu Lys	Glu	Lys Gly	Ala
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Ile Thr	Gln Ser	Pro Leu	Ser	Asp Cys	Leu Thr	Arg	Ser His	Ser
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Ser Phe	Pro Ser	Ile Arg	Pro	Ile Tyr	Leu Thr	Arg	Val Leu	Phe
1415			1420			1425		
Gln Asp	Asn Ser	Ser His	Leu	Pro Ala	Ala Ser	Tyr	Arg Lys	Lys
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Asp Ser	Gly Val	Gln Glu	Ser	Ser His	Phe Leu	Gln	Gly Ala	Lys

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Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp 1490 1495 1500		
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His 1505 1510 1515		
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser 1520 1525 1530		
Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr 1535 1540 1545		
Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val 1550 1555 1560		
Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser 1565 1570 1575		
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln 1580 1585 1590		
Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys 1595 1600 1605		
Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys 1610 1615 1620		
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys 1625 1630 1635		
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg 1640 1645 1650		
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu 1655 1660 1665		
Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr 1670 1675 1680		
Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile 1685 1690 1695		
Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys 1700 1705 1710		
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr 1715 1720 1725		
Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser 1730 1735 1740		
Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr 1745 1750 1755		

Asp Gly 1760	Ser Phe Thr Gln Pro 1765	Leu Tyr Arg Gly Glu 1770	Leu Asn Glu
His Leu 1775	Gly Leu Leu Gly Pro 1780	Tyr Ile Arg Ala Glu 1785	Val Glu Asp
Asn Ile 1790	Met Val Thr Phe Arg 1795	Asn Gln Ala Ser Arg 1800	Pro Tyr Ser
Phe Tyr 1805	Ser Ser Leu Ile Ser 1810	Tyr Glu Glu Asp Gln 1815	Arg Gln Gly
Ala Glu 1820	Pro Arg Lys Asn Phe 1825	Val Lys Pro Asn Glu 1830	Thr Lys Thr
Tyr Phe 1835	Trp Lys Val Gln His 1840	His Met Ala Pro Thr 1845	Lys Asp Glu
Phe Asp 1850	Cys Lys Ala Trp Ala 1855	Tyr Phe Ser Asp Val 1860	Asp Leu Glu
Lys Asp 1865	Val His Ser Gly Leu 1870	Ile Gly Pro Leu Leu 1875	Val Cys His
Thr Asn 1880	Thr Leu Asn Pro Ala 1885	His Gly Arg Gln Val 1890	Thr Val Gln
Glu Phe 1895	Ala Leu Phe Phe Thr 1900	Ile Phe Asp Glu Thr 1905	Lys Ser Trp
Tyr Phe 1910	Thr Glu Asn Met Glu 1915	Arg Asn Cys Arg Ala 1920	Pro Cys Asn
Ile Gln 1925	Met Glu Asp Pro Thr 1930	Phe Lys Glu Asn Tyr 1935	Arg Phe His
Ala Ile 1940	Asn Gly Tyr Ile Met 1945	Asp Thr Leu Pro Gly 1950	Leu Val Met
Ala Gln 1955	Asp Gln Arg Ile Arg 1960	Trp Tyr Leu Leu Ser 1965	Met Gly Ser
Asn Glu 1970	Asn Ile His Ser Ile 1975	His Phe Ser Gly His 1980	Val Phe Thr
Val Arg 1985	Lys Lys Glu Glu Tyr 1990	Lys Met Ala Leu Tyr 1995	Asn Leu Tyr
Pro Gly 2000	Val Phe Glu Thr Val 2005	Glu Met Leu Pro Ser 2010	Lys Ala Gly
Ile Trp 2015	Arg Val Glu Cys Leu 2020	Ile Gly Glu His Leu 2025	His Ala Gly
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Leu Gly 2045	Met Ala Ser Gly His 2050	Ile Arg Asp Phe Gln 2055	Ile Thr Ala

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 2060 2070
 Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser
 2075 2080 2085
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 2090 2095 2100
 Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 2105 2110 2115
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr
 2120 2125 2130
 Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn
 2135 2140 2145
 Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile
 2150 2155 2160
 Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg
 2165 2170 2175
 Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys
 2180 2185 2190
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 Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser
 2210 2215 2220
 Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp
 2225 2230 2235
 Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe
 2240 2245 2250
 Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys
 2255 2260 2265
 Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser
 2270 2275 2280
 Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys
 2285 2290 2295
 Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val
 2300 2305 2310
 Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
 2315 2320 2325
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<211> 1471

<212> DNA

<213> Homo sapiens

<400> 31

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<211> 461

<212> PRT

<213> Homo sapiens

<400> 32

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Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
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Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
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Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
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Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
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Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser

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Val Glu Ala	Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser					
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Asp Ser Ser	Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile					
	370		375		380	
Val Asn Val	Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln					
	385		390		395	
Ala Ser Ser	Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro					
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Lys Asp Glu	Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser					
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Gln Leu Glu	Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro					
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 <212> DNA
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<210> 34
 <211> 431
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
 50 55 60
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
 65 70 75 80
 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
 85 90 95
 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp

	180		185		190
Phe Ala	Ala Ile Tyr Arg Arg His	Arg Gly Gly Ser Val Thr Tyr Val			
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Cys Gly	Gly Ser Leu Ile Ser Pro Cys Trp	Val Ile Ser Ala Thr His			
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Cys Phe	Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	Ile Val Tyr Leu Gly			
	225	230		235	240
Arg Ser	Arg Leu Asn Ser Asn Thr Gln Gly	Glu Met Lys Phe Glu Val			
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Glu Asn	Leu Ile Leu His Lys Asp Tyr Ser	Ala Asp Thr Leu Ala His			
	260	265		270	
His Asn	Asp Ile Ala Leu Leu Lys Ile Arg Ser	Lys Glu Gly Arg Cys			
	275	280		285	
Ala Gln	Pro Ser Arg Thr Ile Gln Thr Ile Cys	Leu Pro Ser Met Tyr			
	290	295		300	
Asn Asp	Pro Gln Phe Gly Thr Ser Cys Glu	Ile Thr Gly Phe Gly Lys			
	305	310		315	320
Glu Asn	Ser Thr Asp Tyr Leu Tyr Pro Glu	Gln Leu Lys Met Thr Val			
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Val Lys	Leu Ile Ser His Arg Glu Cys Gln	Gln Pro His Tyr Tyr Gly			
	340	345		350	
Ser Glu	Val Thr Thr Lys Met Leu Cys Ala	Ala Asp Pro Gln Trp Lys			
	355	360		365	
Thr Asp	Ser Cys Gln Gly Asp Ser Gly Gly	Pro Leu Val Cys Ser Leu			
	370	375		380	
Gln Gly	Arg Met Thr Leu Thr Gly Ile Val	Ser Trp Gly Arg Gly Cys			
	385	390		395	400
Ala Leu	Lys Asp Lys Pro Gly Val Tyr Thr	Arg Val Ser His Phe Leu			
	405	410		415	
Pro Trp	Ile Arg Ser His Thr Lys Glu Glu	Asn Gly Leu Ala Leu			
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Asp Arg	Val Thr Ile Thr Cys Arg Ala	Ser Gln Asp Val Asn Thr Ala			
	20	25		30	
Val Ala	Trp Tyr Gln Gln Lys Pro Gly	Lys Ala Pro Lys Leu Leu Ile			
	35	40		45	

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Thr Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 36
<211> 120
<212> PRT
<213> Mus musculus

<400> 36
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 37
<211> 120
<212> PRT
<213> Mus musculus

<400> 37
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120
 <210> 38
 <211> 106
 <212> PRT
 <213> Mus musculus
 <400> 38
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 39
 <211> 1039
 <212> DNA
 <213> Homo sapiens
 <400> 39
 tcctgcacag gcagtgccct gaagtgcctc ttcagagacc tttcttcata gactactttt 60
 tttttcttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120
 cattctcgtc atctctgagg acatcaccat catctcagga tgagggggcat gaagctgctg 180
 ggggcgtgc tggcactggc ggcctactg cagggggccg tgtccctgaa gatcgagcc 240
 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300
 gtgcagatcc tgagccgcta tgacatcgcc ctgggtccagg aggtcagaga cagccacctg 360
 actgcctgtg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420
 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480

cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg 540
 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctccgggtt cacagaggtc, 600
 agggagtttg ccaattgttc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 660
 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg 720
 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 780
 ctgtggacaa gcccaccctt ccagtggctg atccccgaca gcgctgacac cacagctaca 840
 cccagccact gtgcctatga caggatcgctg gttgcaggga tgctgctcgg aggcgcggtt 900
 gttcccgact cggctcttcc cttaacttc caggctgcct atggcctgag tgaccaactg 960
 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgcgc agcccctccc 1020
 cacaccagtt gaactgcag 1039

<210> 40

<211> 282

<212> PRT

<213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
100 105 110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys
275 280

<210> 41
<211> 678
<212> DNA
<213> Mus musculus

<400> 41
gacatcttgc tgactcagtc tccagccatc ctgtctgtga gtccaggaga aagagtcagt 60
ttctcttcca gggccagtc gttcgttggc tcaagcatcc actggtatca gcaagaaca 120
aatggtcttc caagccttct cataaagtat gttcttgagt ctatgtctgg gatcccttc 180
aggtttagtg gcagtggtgc agggacagat tttactctta gcatcaaac tgtggagtct 240
gaagatattg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg 300
gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa 360
cctggaggat coactgaaact ctctgtgttt gcctctggat tcatittcag taacctctgg 420
atgaactggg tccgccagtc tccagagaag gggottgagt gggttgctga aattagatca 480
aaatctatta attctgcaac acattatgcg gagtctgtga aaggagggtt caccatctca 540
agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact 600
ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggc 660
accactctca cagtctcc 678

<210> 42
<211> 226
<212> PRT
<213> Mus musculus

<400> 42
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
 35 40 45
 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
 65 70 75 80
 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
 85 90 95
 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
 100 105 110
 Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
 115 120 125
 Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
 130 135 140
 Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
 145 150 155 160
 Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
 165 170 175
 Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
 180 185 190
 Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
 195 200 205
 Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
 210 215 220

Val Ser
225

<210> 43
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 43
 gctgcatcag aagaggccat caagcacatc actgtccctc tgccatggcc ctgtggatgc 60
 gccctctgcc cctgctggcg ctgctggccc tctggggacc tgacccagcc gcagccttgy 120
 tgaaccaaca cctgtggcgc toacacctgg tggaagetct ctacctagtg tgcgggggaa 180
 gaggtctctt ctacacaccc aagaccgccg gggaggcaga ggacctgcag gtggggcgag 240
 tggagctggg cggggggccct ggtgcaggca gccctgcagcc cttggccctg gaggggtccc 300
 tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg 360
 agaactactg caactagacg cagcccgcag gcagccccc acccgccgcc tctgacacg 420
 agagagatgg aataaagccc ttgaaccagc 450

<210> 44
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
 1 5 10 15
 Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
 20 25 30
 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
 35 40 45
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
 50 55 60
 Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
 65 70 75 80
 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
 85 90 95
 Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
 100 105 110

<210> 45
 <211> 1203
 <212> DNA
 <213> Hepatitis B virus

<400> 45
 atgggagggtt ggtcttccaa acctcgacaa ggcattggga cgaatcttct tgttccaat 60
 cctctgggat tctttccoga tcaccagttg gacctcggt tcggagccaa ctcaacaat 120
 ccagattggg acttcaacc caacaaggat cactggccag aggcaatcaa ggtaggagcg 180
 ggagacttcg ggccagggtt caccaccca caccggcgtc ttttgggtg gagccctcag 240
 gctcagggca tattgacaac agtgccagca gcgcctctc ctgtttccac caatcggaag 300
 tcaggaagac agcctactcc catctctcca cctctaagag acagtcatcc tcaggccatg 360
 cagtgaact ccacaacatt ccaccaagct ctgctagatc ccagagttag ggcctatat 420
 tttcctgctg gtggctccag ttccggaaca gttaaaccctg ttccgactac tgtctcacc 480
 atatcgtaaa tcttctcgag gactggggac cctgcacoga acatggagag cacaacatca 540
 ggattcttag gacctgct cgtgttacag gcggggtttt tcttgttagc aagaatctc 600
 acaataccac agagtctaga ctggtggtg acttctctca attttctagg gggagcacc 660
 acgtgtcctg gccaaaattc gcagtcacca acctccaatc actcaccac ctctgttct 720
 ccaatttgct ctggttatcg ctggatgtgt ctgcggcggt ttatcatatt cctcttcac 780
 ctgctgtat gccctatctt cttgttggtt cttctggact accaaggtag gttgcccggt 840

tgtcctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt 900
 cctgctcaag gaacctctat gtttccctct tgggtgctga caaaaccttc ggacggaac 960
 tgcacttgta ttcccatccc atcactctgg gctttcgcaa gattcctatg ggagtgaggc 1020
 tcagtcggtt tctcctggct cagtttacta gtgcatttg ttcagtgggt cgcagggctt 1080
 tccccactg tttggcttcc agttatatgg atgatgtggt attgggggcc aagtcgtac 1140
 aacatcttga gtcccttttt acctctatta ccaattttct tttgtctttg ggtatacatt 1200
 tga 1203

<210> 46
 <211> 400
 <212> PRT
 <213> Hepatitis B virus

<400> 46
 Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
 1 5 10 15
 Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30
 Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45
 Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60
 Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80
 Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95
 Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110
 Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125
 Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140
 Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160
 Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175
 Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190
 Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205
 Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240
 Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 245 250 255
 Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 260 265 270
 Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 275 280 285
 Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 290 295 300
 Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
 305 310 315 320
 Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
 325 330 335
 Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
 340 345 350
 Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
 355 360 365
 Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
 370 375 380
 Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 385 390 395 400

<210> 47

<211> 799

<212> DNA

<213> Homo sapiens

<400> 47

cgaaccactc agggctcctgt ggacagctca cctagctgca atggctacag gctcccgga 60
 gtccctgctc ctggcttttg gctgctctg cctgacctgg cttcaagagg gcagtgacct 120
 cccaaccatt cccttatcca ggccttttga caacgctatg ctcgcgcgcc atcgtctgca 180
 ccagctggcc tttagacact accaggagtt tgaagaagcc tatatccaa aggaacagaa 240
 gtattcatct ctgcagaacc ccagacctc cctctgtttc tcagagtcta ttccgacacc 300
 ctccaacagg gaggaaacac aacagaaatc caacctagag ctgctccgca tctcctgct 360
 gctcatccag tcgtggctgg agcccgctga gttcctcagg agtgccttcg ccaacagcct 420
 ggtgtacggc gctctgaca gcaacgtcta tgacctcta aaggacctag aggaaggcat 480
 ccaaacgctg atggggaggc tggaagatgg cagcccccg actgggcaga tcttcaagca 540
 gacctacagc aagttcgaca caaactcaca caacgatgac gcactactca agaactacgg 600
 gctgctctac tgcttcagga aggacatgga caaggtcgag acattcctgc gcagtgtgca 660

gtgccgctct gtggagggca gctgtggctt ctatgtgccc gggtaggcac cctgtgaccc 720
 cteccacgtg cctctcctgg ccttggaagt tgccactcca gtgcccacca gccctgtcct 780
 aataaaatta agttgcatc 799

<210> 48
 <211> 217
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1 5 10 15
 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
 20 25 30
 Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
 35 40 45
 Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
 50 55 60
 Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
 65 70 75 80
 Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
 85 90 95
 Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
 100 105 110
 Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
 115 120 125
 Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
 130 135 140
 Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
 145 150 155 160
 Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
 165 170 175
 His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
 180 185 190
 Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
 195 200 205
 Arg Ser Val Glu Gly Ser Cys Gly Phe
 210 215

<210> 49
 <211> 963
 <212> DNA
 <213> Homo sapiens

<400> 49

atggagacag acacactcct gttatgggtg ctgctgtctt gggttccagg ttccactggt 60
gacgtcaggc gagggcccg gagcctgcgg ggcaggggacg cgcacagccc caccgccctgc 120
gtcccggcgg agtgcttcga cctgctgtgc cgcactgcgg tggcctgcgg gctcctgcgc 180
acgcccgccg cgaacccggc cggggccagc agccctgcgc ccaggacggc gctgcagccg 240
caggagtccg tgggcgcggg ggccggcgag gcggcggtcg acaaaactca cacatgccca 300
ccgtgcccg caccctgaact cctgggggga ccgtcagttt tcctcttccc cccaaaaccc 360
aaggacaccc tcattgatctc ccggaccctt gaggtcacat gcgtggtggt ggacgtgagc 420
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 480
aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 540
gtcctgcacc aggactggct gaatggcaag gactacaagt gcaaggtctc caacaaagcc 600
ctccagcccc ccactcgaga aaccatctcc aaagccaaag ggcagccccg agaaccacag 660
gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 720
ctgggtcaaag gctttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 780
gagaacaact acaagaccac gcctcccgtg ttggactccg acggctcctt cttcctctac 840
agcaagctca ccgtggacaa gagcagggtg cagcagggga acgtctcttc atgtccgtg 900
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tcccgggaaa 960
tga 963

<210> 50

<211> 320

<212> PRT

<213> Homo sapiens

<400> 50

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg
20 25 30

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
35 40 45

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
50 55 60

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
65 70 75 80

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
85 90 95

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
100 105 110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 115 120 125
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 130 135 140
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 145 150 155 160
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 165 170 175
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 180 185 190
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 195 200 205
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 210 215 220
 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 225 230 235 240
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 245 250 255
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 260 265 270
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 275 280 285
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 290 295 300
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 305 310 315 320
 <210> 51
 <211> 107
 <212> FRT
 <213> Homo sapiens
 <400> 51
 Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp

85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
 100 105
 <210> 52
 <211> 107
 <212> PRT
 <213> Mus musculus
 <400> 52
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80
 Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95
 Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 100 105
 <210> 53
 <211> 119
 <212> PRT
 <213> Homo sapiens
 <400> 53
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30
 Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 54
 <211> 119
 <212> PRT
 <213> Mus musculus

<400> 54
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr
 1 5 10 15
 Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30
 Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ala
 115

<210> 55
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 55
 Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95
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 <213> Mus musculus

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384

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 <211> 128
 <212> PRT
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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
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 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
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 Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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 <213> Mus musculus

<400> 62
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 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
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 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
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 Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
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 130 135 140

<210> 63
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 <213> Homo sapiens

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<211> 464

<212> PRT

<213> Homo sapiens

<400> 64

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Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
 50 55 60

Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
 65 70 75 80

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
 85 90 95

His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
 100 105 110

Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
 115 120 125

Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
 130 135 140

Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
 145 150 155 160

Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
 165 170 175

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 180 185 190

Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys

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<210> 65

<211> 1962

<212> DNA

<213> Homo sapiens

<400> 65

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<210> 66
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 <212> PRT
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 <400> 66
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 35 40 45

 Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
 50 55 60

 Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
 65 70 75 80

 Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
 85 90 95

 Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
 100 105 110

 His Leu Asp Gly Tyr Leu Asp Leu Arg Glu Asn Gln Leu Leu Pro
 115 120 125

 Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
 130 135 140

 Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
 145 150 155 160

 Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
 165 170 175

 Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
 180 185 190

 Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
 195 200 205

 Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
 210 215 220

 Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
 225 230 235 240

 Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
 245 250 255

 Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
 260 265 270

 Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
 275 280 285

 Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val

290	295	300
Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala 305 310 315 320		
Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn 325 330 335		
Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe 340 345 350		
Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg 355 360 365		
Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys 370 375 380		
Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln 385 390 395 400		
Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His 405 410 415		
Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp 420 425 430		
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala 435 440 445		
His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro 450 455 460		
Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu 465 470 475 480		
Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro 485 490 495		
Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala 500 505 510		
Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro 515 520 525		
Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro 530 535 540		
Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr 545 550 555 560		
Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys 565 570 575		
Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr 580 585 590		
Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser 595 600 605		
Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp 610 615 620		

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
645 650

<210> 67
<211> 1290
<212> DNA
<213> Homo sapiens

<400> 67
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ctcgtttcct gggacatccc tggggctaga gcactggaca atggattggc aaggacgcct 120
accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgccca ggaagagcca 180
gattcctgca tcagtgagaa gctcttcagt gagatggcag agctcatggt ctcagaaggc 240
tggaaggatg cagggttatga gtacctctgc attgatgact gttggatggc tccccaaga 300
gattcagaag gcagacttca ggcagaccct cagcgctttc ctcattggat togccagcta 360
gctaattatg ttacacagca aggactgaag ctagggtatt atgcagatgt tggaaataaa 420
acctgcgcag gcttccctcg gagttttgga tactacgaca ttgatccca gacctttgct 480
gactggggag tagatctgct aaaatttgat ggttgttact gtgacagttt ggaaaaattg 540
gcagatggtt ataagcacat gtccttgcc ctgaatagga ctggcagaag cattgtgtac 600
tctgtgagt ggcctcttta tatgtggccc ttcaaaagc ccaattatac agaaatccga 660
cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag 720
agtatcttgg actggacatc tttaaccag gagagaattg ttgatgttgc tggaccaggg 780
ggttggaatg acccagatat gttagtalt ggcaactttg gcctcagctg gaatcagcaa 840
gtaactcaga tggcctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc 900
cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat 960
caggccccct tgggcaagca aggtaccag cttagacagg gagacaactt tgaagtgtgg 1020
gaacgccttc tctcaggctt agcctgggct gtactgtatga taaaccggca ggagattggt 1080
ggacctcgct cttataccat cgcagtgtct tccctgggta aaggagtggc ctgtaactct 1140
gcctgtttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaattgact 1200
tcaaggttaa gaagtcacat aaatoccaca ggcactgttt tgcttcagct agaaaaatac 1260
atgcagatgt cattaataa cttactttaa 1290

<210> 68
<211> 429
<212> PRT
<213> Homo sapiens

<400> 68
 Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
 1 5 10 15
 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110
 Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
 115 120 125
 Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
 130 135 140
 Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
 145 150 155 160
 Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
 165 170 175
 Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
 180 185 190
 Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
 195 200 205
 Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
 210 215 220
 His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
 225 230 235 240
 Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
 245 250 255
 Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
 260 265 270
 Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
 275 280 285
 Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
 290 295 300
 Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
 305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
355 360 365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
370 375 380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385 390 395 400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
405 410 415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
420 425

<210> 69

<211> 351

<212> DNA

<213> Homo sapiens

<400> 69

atggattact acagaaaata tgcagctatc tttctggtca cattgtcgggt gtttctgcat 60

gttctccatt cgcgtcctga tgtgcaggat tgccagaat gcacgtaca ggaaaaacca 120

ttcttctccc agcgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca 180

tatcccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag 240

tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg tttcaaagtg 300

gagaaccaca cggtgtgcca ctgcagtact tggtattatc acaaatctta a 351

<210> 70

<211> 116

<212> PRT

<213> Homo sapiens

<400> 70

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1 5 10 15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
20 25 30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
35 40 45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
50 55 60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65 70 75 80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
 85 90 95
 Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
 100 105 110

Tyr His Lys Ser
 115

<210> 71
 <211> 498
 <212> DNA
 <213> Homo sapiens

<400> 71
 atggagatgt tccaggggct gctgctgttg ctgctgctga gcatgggagg gacatgggca 60
 tccaaggagc cgcttcggcc acggtgccgc cccatcaatg ccaccctggc tgtggagaag 120
 gagggctgcc ccgtgtgcat caccgtcaac accaccatct gtgcgggcta ctgccccacc 180
 atgacccgcg tgctgcaggg ggtcctgcgc gccctgcctc aggtgggtgtg caactaccgc 240
 gatgtgcgct tcgagtcacat ccgggtccct ggctgccgcg gcggcgtaaa ccccggtggtc 300
 tcctacgcgc tggtctctcag ctgtcaatgt gaactctgcc gccgcagcac cactgactgc 360
 ggggggccca aggaccacc cttgacctgt gatgaccccc gcttcaggga ctctctcttc 420
 tcaaaggccc ctccccccag ccttccaagc ccateccgac tcccggggcc ctcgagacac 480
 ccgactctcc cacaataa 498

<210> 72
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 72
 Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Ser Met Gly
 1 5 10 15
 Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
 20 25 30
 Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
 35 40 45
 Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
 50 55 60
 Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
 65 70 75 80
 Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
 85 90 95
 Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
 100 105 110
 Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu

115 120 T25
 Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro
 130 135 140
 Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
 145 150 155 160
 Pro Ile Leu Pro Gln
 165

<210> 73
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 73
 Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1 5 10 15
 Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 20 25 30
 Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 35 40 45
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
 50 55 60
 Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
 65 70 75 80
 Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 85 90 95
 Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 100 105 110
 Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 115 120 125
 Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 130 135 140
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 145 150 155 160
 Cys Arg Thr Gly Asp
 165

<210> 74
 <211> 588
 <212> DNA
 <213> Homo sapiens

<400> 74
 atggccctcc tgttccctct actggcagcc ctagtgatga ccagctatag cctctgttga 60
 tctctgggct gtgactctgcc tcagaacctt ggctacttta gcaggaacac ctgtgtgctt 120
 ctgcacaaaa tgaggagaat ctcccctttc ttgtgtctca aggacagaag agacttcagg 180

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ttccccagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtctctc 240
catgagatgc tgcagcagat cttcagcctc ttccacacag agcgtctctc tgctgtcctgg 300
aacatgaccc tcttagacca actccacact ggacttcctc agcaactgca acacctggag 360
acctgcttgc tgcaggtagt gggagaagga gaatctgctg gggcaattag cagccctgca 420
ctgaccttga ggaggtactt ccagggaatc cgtgtctacc tgaagagaa gaaatacagc 480
gactgtgcct gggaagtgtt cagaatggaa atcatgaaat ccttgttctt atcaacaac 540
atgcaagaaa gactgagaag taaagataga gacctgggct catcttga 588

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<210> 75
<211> 195
<212> PRT
<213> Homo sapiens

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<400> 75
Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
180 185 190

Gly Ser Ser
195

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